GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:04 ; Search time 23 Seconds
(without alignments)
425.583 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264
Sequence: 1 MTGYEARLITFGTWMYSVNK.....VDRCPMCSAVIDFKQRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1264	100.0	236	1	BIR8_HUMAN	Q96p09 homo sapien
2	1241	98.2	236	1	BIR8_PANTR	Q95m72 pan troglod
3	1237	97.9	236	1	BIR8_GORGO	Q95m71 gorilla gor
4	1052	83.2	497	1	BIR4_HUMAN	P98170 homo sapien
5	1029	81.4	496	1	BIR4_RAT	Q9r0i6 rattus norv
6	1028	81.3	496	1	BIR4_MOUSE	Q60989 mus musculu
7	472.5	37.4	604	1	BIR2_HUMAN	Q13489 homo sapien
8	458.5	36.3	618	1	BIR3_HUMAN	Q13490 homo sapien
9	455.5	36.0	600	1	BIR2_MOUSE	O08863 mus musculu
10	454.5	36.0	611	1	BIR_CHICK	Q90660 gallus gall
11	443	35.0	612	1	BIR3_MOUSE	Q62210 mus musculu
12	427	33.8	358	1	PIAP_PIG	O62640 sus scrofa
13	401	31.7	498	1	IAP2_DROME	Q24307 drosophila
14	373.5	29.5	298	1	BIR7_HUMAN	Q96ca5 homo sapien
15	335	26.5	438	1	IAP1_DROME	Q24306 drosophila
16	314.5	24.9	275	1	IAP_GVCP	P41436 cydia pomon
17	312.5	24.7	268	1	IAP3_NPVOP	P41437 orgyia pseu
18	228.5	18.1	1403	1	BIRE_MOUSE	Q9r016 mus musculu
19	223.5	17.7	1403	1	BIRF_MOUSE	Q9jib6 mus musculu
20	222.5	17.6	1402	1	BIRG_MOUSE	Q9jib3 mus musculu
21	222.5	17.6	1447	1	BIRB_MOUSE	Q9quk4 mus musculu
22	218.5	17.3	1403	1	BIRA_MOUSE	Q9qwk5 mus musculu
23	209.5	16.6	1403	1	BIR1_HUMAN	Q13075 homo sapien
24	206.5	16.3	239	1	ZFP_IRV6	P47732 chilo iride
25	184	14.6	286	1	IAP1_NPVAC	P41435 autographa
26	182	14.4	275	1	IAP1_NPVOP	O10296 orgyia pseu
27	165.5	13.1	249	1	IAP2_NPVAC	P41454 autographa
28	134	10.6	142	1	BIR5_RAT	Q9jhy7 rattus norv
29	132	10.4	140	1	BIR5_MOUSE	O70201 mus musculu
30	130	10.3	142	1	BIR5_HUMAN	O15392 homo sapien
31	127.5	10.1	4829	1	BIR6_HUMAN	Q9nr09 homo sapien
32	126	10.0	145	1	ZEF2_IRV6	P40629 chilo iride
33	111	8.8	433	1	RN26_HUMAN	Q9by78 homo sapien
34	109.5	8.7	489	1	MDM4_MOUSE	O35618 mus musculu
35	108	8.5	487	1	MDM2_CANFA	P56950 canis famil
36	106.5	8.4	224	1	IAPL_ASFM1	O11452 african swi
37	104.5	8.3	224	1	IAPL_ASFB7	Q65138 african swi
38	104.5	8.3	490	1	MDM4_HUMAN	O15151 homo sapien
39	104	8.2	491	1	MDM2_HORSE	P56951 equus cabal
40	102	8.1	236	1	IAP2_NPVOP	O10324 orgyia pseu
41	100.5	8.0	224	1	IAPL_ASFCH	O12407 african swi
42	98	7.8	473	1	MDM2_XENLA	P56273 xenopus lae
43	98	7.8	539	1	Z173_HUMAN	Q12899 homo sapien
44	96.5	7.6	224	1	IAPL_ASFC3	O11451 african swi
45	96	7.6	491	1	MDM2_HUMAN	Q00987 homo sapien

ALIGNMENTS

RESULT 1
BIR8_HUMAN
ID BIR8_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIRC8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and
RT identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SUBUNIT: Binds to caspase-9.
CC -!- TISSUE SPECIFICITY: Testis-specific in normal tissues.
CC -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC ---

CC ---
DR EMBL; AF420440; AAL30369.1; -.
DR EMBL; AF164682; AAK81892.1; -.
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.

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DR   PROSITE; PS01282; BIR_REPEAT_1; 1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger.
FT   REPEAT       7     70       BIR.
FT   ZN_FING     189    224      RING-TYPE.
FT   CONFLICT    196    196      Y -> H (IN REF. 2).
SQ   SEQUENCE   236 AA;  27115 MW;  CB7F034B0DDFAD9D CRC64;

  Query Match             100.0%;  Score 1264;  DB 1;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-94;
  Matches  236;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 2
BIR8_PANTR
ID   BIR8_PANTR     STANDARD;      PRT;   236 AA.
AC   Q95M72;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE   like protein 2) (IAP-like protein 2) (ILP-2).
GN   BIRC8 OR ILP2.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286921; PubMed=11390657;
RA   Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA   Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA   Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT   "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT   apoptosis protein family.";
RL   Mol. Cell. Biol. 21:4292-4301(2001).
CC   -!- FUNCTION: Protects against apoptosis mediated by BAX (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY030052; AAK49776.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger.
FT   REPEAT       7     70       BIR.
FT   ZN_FING     189    224      RING-TYPE.
SQ   SEQUENCE   236 AA;  27136 MW;  64CCA3A251420EDE CRC64;

  Query Match             98.2%;  Score 1241;  DB 1;  Length 236;
  Best Local Similarity   97.9%;  Pred. No. 9e-93;
  Matches  231;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYFVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRINDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENESNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||:||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQDEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 3
BIR8_GORGO
ID   BIR8_GORGO     STANDARD;      PRT;   236 AA.
AC   Q95M71;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE   like protein 2) (IAP-like protein 2) (ILP-2).
GN   BIRC8 OR ILP2.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286921; PubMed=11390657;
RA   Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA   Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA   Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT   "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT   apoptosis protein family.";
RL   Mol. Cell. Biol. 21:4292-4301(2001).
CC   -!- FUNCTION: Protects against apoptosis mediated by BAX (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY030053; AAK49777.1; -.
DR   InterPro; IPR001370; BIR.
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DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger.
FT   REPEAT       7     70       BIR.
FT   ZN_FING     189    224      RING-TYPE.
SQ   SEQUENCE   236 AA;  27120 MW;  C3A70E39EE442E4C CRC64;

  Query Match             97.9%;  Score 1237;  DB 1;  Length 236;
  Best Local Similarity   97.0%;  Pred. No. 1.9e-92;
  Matches  229;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |||||| |||||||||||||||||||||||||||||:||||||||||||||||||||||
Db          1 MTGYEAWLITFGTWMYSVNKEQLARAGFYAIGQEDKIQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||||||:||||||:|||||||||||||||||||||||||||| ||||||||||||||||
Db        121 MGFDFKDIKKIMEEKIQTSGSNYKTLEVLVADLVSAQKDTTENESNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||||:|||||||||||||||||||||||||:||||||||||||
Db        181 RRLQEEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCNAVIDFKQRVFMS 236


RESULT 4
BIR4_HUMAN
ID   BIR4_HUMAN     STANDARD;      PRT;   497 AA.
AC   P98170; Q9NQ14;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE   protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE   (IAP-like protein) (HILP).
GN   BIRC4 OR API3 OR IAP3 OR XIAP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=96149249; PubMed=8552191;
RA   Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA   Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT   "Suppression of apoptosis in mammalian cells by NAIP and a related
RT   family of IAP genes.";
RL   Nature 379:349-353(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal heart;
RX   MEDLINE=96256286; PubMed=8654366;
RA   Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA   Gilfillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;
RT   "A conserved family of cellular genes related to the baculovirus iap
RT   gene and encoding apoptosis inhibitors.";
RL   EMBO J. 15:2685-2694(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Grafham D.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   MEDLINE=97373959; PubMed=9230442;
RA   Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT   "X-linked IAP is a direct inhibitor of cell-death proteases.";
RL   Nature 388:300-304(1997).
RN   [5]
RP   MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX   MEDLINE=21634829; PubMed=11604410;
RA   Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA   Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
RA   Simpson R.J., Vaux D.L.;
RT   "HtrA2 promotes cell death through its serine protease activity and
RT   its ability to antagonize inhibitor of apoptosis proteins.";
RL   J. Biol. Chem. 277:445-454(2002).
RN   [6]
RP   STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX   MEDLINE=21020961; PubMed=11140637;
RA   Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
RA   Herrmann J., Wu J.C., Fesik S.W.;
RT   "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
RT   domain.";
RL   Nature 408:1004-1008(2000).
CC   -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD
CC       LEUKOCYTES.
CC   -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC       and -7, while the third BIR is involved in caspase-9 inhibition.
CC       The interactions with SMAC and PRSS25 are mediated by the second
CC       and third BIR domains.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; U45880; AAC50373.1; -.
DR   EMBL; U32974; AAC50518.1; -.
DR   EMBL; AL121601; CAB95312.1; -.
DR   PDB; 1G3F; 10-JAN-01.
DR   Genew; HGNC:592; BIRC4.
DR   MIM; 300079; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW   3D-structure.
FT   REPEAT       26     93       BIR 1.
FT   REPEAT      163    230       BIR 2.
FT   REPEAT      265    330       BIR 3.
FT   ZN_FING     450    485       RING-TYPE.
FT   MUTAGEN     214    214       D->S: REDUCED INTERACTION WITH PRSS25.
FT   MUTAGEN     314    314       E->S: DECREASED INTERACTION WITH SMAC AND
FT                                WITH PRSS25.
FT   CONFLICT    162    162       S -> C (IN REF. 1).
FT   CONFLICT    423    423       Q -> P (IN REF. 2).
SQ   SEQUENCE   497 AA;  56684 MW;  9D394C16D45EB635 CRC64;

  Query Match             83.2%;  Score 1052;  DB 1;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 3.3e-77;
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  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:||||||||:|||| ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:||||||||||||||||:|||| || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 5
BIR4_RAT
ID   BIR4_RAT       STANDARD;      PRT;   496 AA.
AC   Q9R0I6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE   protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE   (IAP homolog A) (RIAP3) (RIAP-3).
GN   BIRC4 OR API3 OR XIAP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Saito N.;
RT   "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC       (By similarity).
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC       and -7, while the third BIR is involved in caspase-9 inhibition.
CC       The interactions with SMAC and PRSS25 are mediated by the second
CC       and third BIR domains (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB033366; BAA85304.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT       26     93       BIR 1.
FT   REPEAT      163    230       BIR 2.
FT   REPEAT      264    329       BIR 3.
FT   ZN_FING     449    484       RING-TYPE.
SQ   SEQUENCE   496 AA;  56072 MW;  E250E3C77461A469 CRC64;

  Query Match             81.4%;  Score 1029;  DB 1;  Length 496;
  Best Local Similarity   76.7%;  Pred. No. 2.3e-75;
  Matches  181;  Conservative   33;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  |:||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        261 MAEYDARIVTFGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:||| |||||||||| ||  ::|:| :||||:||:| |||| |||:|||||
Db        321 KWYPGCKYLLDEKGQEYINNIHLTHSLGESVVRTAEKTPSVTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||:|||:|| |||::|||||| :||||:||||||||| :::| :|||||::|| || |
Db        381 MGFNFKDIKKTMEEKLQTSGSNYLSLEVLIADLVSAQKDNSQDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:||||||||||||||||:|||| || |||::|||
Db        441 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCCTVITFKQKIFMS 496


RESULT 6
BIR4_MOUSE
ID   BIR4_MOUSE     STANDARD;      PRT;   496 AA.
AC   Q60989; O08865;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE   protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE   (IAP homolog A) (MIAP3) (MIAP-3).
GN   BIRC4 OR API3 OR XIAP OR AIPA OR MIHA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX   MEDLINE=96209843; PubMed=8643514;
RA   Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT   "Cloning and expression of apoptosis inhibitory protein homologs that
RT   function to inhibit apoptosis and/or bind tumor necrosis factor
RT   receptor-associated factors.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC       (By similarity).
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC       and -7, while the third BIR is involved in caspase-9 inhibition.
CC       The interactions with SMAC and PRSS25 are mediated by the second
CC       and third BIR domains (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; U36842; AAC52594.1; -.
DR   EMBL; U88990; AAB58376.1; -.
DR   HSSP; Q13490; 1QBH.
DR   MGD; MGI:107572; Birc4.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT       26     93       BIR 1.
FT   REPEAT      163    230       BIR 2.
FT   REPEAT      264    329       BIR 3.
FT   ZN_FING     449    484       RING-TYPE.
FT   CONFLICT    208    208       E -> K (IN REF. 2).
FT   CONFLICT    317    317       E -> D (IN REF. 2).
FT   CONFLICT    322    322       W -> C (IN REF. 2).
FT   CONFLICT    346    346       S -> P (IN REF. 2).
FT   CONFLICT    360    360       S -> P (IN REF. 2).
FT   CONFLICT    388    388       I -> L (IN REF. 2).
FT   CONFLICT    449    449       C -> S (IN REF. 2).
FT   CONFLICT    462    462       V -> F (IN REF. 2).
FT   CONFLICT    468    468       V -> A (IN REF. 2).
FT   CONFLICT    490    490       K -> N (IN REF. 2).
SQ   SEQUENCE   496 AA;  56079 MW;  EC5FAE0799F2CDD8 CRC64;

  Query Match             81.3%;  Score 1028;  DB 1;  Length 496;
  Best Local Similarity   78.4%;  Pred. No. 2.7e-75;
  Matches  185;  Conservative   26;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||  |||||||||||||||:|: |||:||||||||  :||| ||||||||
Db        261 MAEYEARIVTFGTWTSSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||:||| |||||||||| ||| :| :| :|||||||:| |||| |||:|||||
Db        321 KWYPGCKYLLDEKGQEYINNIHLTHSLEESLGRTAEKTPSLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:||||||:| :||||:|||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDIKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||::|||
Db        441 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 496


RESULT 7
BIR2_HUMAN
ID   BIR2_HUMAN     STANDARD;      PRT;   604 AA.
AC   Q13489; Q16628; Q9UP46; Q9HC27;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis
DE   protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex
DE   protein 1) (IAP homolog C).
GN   BIRC2 OR API1 OR IAP1 OR MIHC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96128127; PubMed=8548810;
RA   Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT   "The TNFR2-TRAF signaling complex contains two novel proteins related
RT   to baculoviral inhibitor of apoptosis proteins.";
RL   Cell 83:1243-1252(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=96149249; PubMed=8552191;
RA   Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA   Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT   "Suppression of apoptosis in mammalian cells by NAIP and a related
RT   family of IAP genes.";
RL   Nature 379:349-353(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=96209843; PubMed=8643514;
RA   Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT   "Cloning and expression of apoptosis inhibitory protein homologs that
RT   function to inhibit apoptosis and/or bind tumor necrosis factor
RT   receptor-associated factors.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99252096; PubMed=10233894;
RA   Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA   ten Cate J.W., Pannekoek H.;
RT   "Vascular endothelial genes that are responsive to tumor necrosis
RT   factor-alpha in vitro are expressed in atherosclerotic lesions,
RT   including inhibitor of apoptosis protein-1, stannin, and two novel
RT   genes.";
RL   Blood 93:3418-3431(1999).
RN   [5]
RP   SEQUENCE OF 362-441 FROM N.A.
RX   MEDLINE=20519161; PubMed=11066071;
RA   Baens M., Steyls A., Dierlamm J., De Wolf-Peeters C., Marynen P.;
RT   "Structure of the MLT gene and molecular characterization of the
RT   genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT   B-cell lymphomas of MALT type.";
RL   Genes Chromosomes Cancer 29:281-291(2000).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC       WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC       FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC       NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC       THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC       INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC   -!- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC       recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC       tissue). This translocation is found in approximately 50% of
CC       cytogenetically abnormal low-grade MALT lymphoma and involves
CC       MALT1 and BIRC2.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ------------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; L49432; AAC41943.1; -.
DR   EMBL; U45878; AAC50371.1; -.
DR   EMBL; U37546; AAC50507.1; -.
DR   EMBL; AF070674; AAC83232.1; -.
DR   EMBL; AF178945; AAG09369.1; -.
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DR   HSSP; Q13490; 1QBH.
DR   Genew; HGNC:591; BIRC3.
DR   MIM; 601712; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
FT   REPEAT       29     96       BIR 1.
FT   REPEAT      169    235       BIR 2.
FT   REPEAT      255    322       BIR 3.
FT   DOMAIN      439    529       CARD.
FT   ZN_FING     557    592       RING-TYPE.
FT   SITE        442    443       BREAKPOINT FOR TRANSLOCATION TO FORM
FT                                BIRC2-MALT1.
FT   CONFLICT     18     18       N -> Y (IN REF. 4).
FT   CONFLICT    119    119       N -> H (IN REF. 2).
FT   CONFLICT    153    153       D -> E (IN REF. 2).
FT   CONFLICT    163    163       H -> P (IN REF. 2).
FT   CONFLICT    165    165       A -> P (IN REF. 2).
FT   CONFLICT    191    191       K -> R (IN REF. 2).
FT   CONFLICT    364    364       F -> L (IN REF. 2).
FT   CONFLICT    552    552       Q -> P (IN REF. 2).
SQ   SEQUENCE   604 AA;  68371 MW;  8581A00BA9AAB4A7 CRC64;

  Query Match             37.4%;  Score 472.5;  DB 1;  Length 604;
  Best Local Similarity   31.0%;  Pred. No. 1.4e-30;
  Matches  111;  Conservative   40;  Mismatches   80;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||  ||  |  |  || |||| |||| :|  | |:|| | |||  |:  :||| |
Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106
              ||||:| |:||:  || |:|  :     ||   |     :|  :|      |
Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHFEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159
                   | |  | |::  |: |||    ||: :: :|  :| ||: :  || ||::|: :
Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN---------------------------------------------- 166
                      | | | |
Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ-----------------------------------------------REISPEE 178
              |||||                                               ::  ||
Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||||| ||:||| ::::|||||||| || || :: :||:| : |    | |:|
Db        547 QLRRLQEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604


RESULT 8
BIR3_HUMAN
ID   BIR3_HUMAN     STANDARD;      PRT;   618 AA.
AC   Q13490; Q16516;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
DE   protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE   protein 2) (IAP homolog B).
GN   BIRC3 OR API2 OR IAP2 OR MIHB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96128127; PubMed=8548810;
RA   Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT   "The TNFR2-TRAF signaling complex contains two novel proteins related
RT   to baculoviral inhibitor of apoptosis proteins.";
RL   Cell 83:1243-1252(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=96149249; PubMed=8552191;
RA   Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA   Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT   "Suppression of apoptosis in mammalian cells by NAIP and a related
RT   family of IAP genes.";
RL   Nature 379:349-353(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=96209843; PubMed=8643514;
RA   Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT   "Cloning and expression of apoptosis inhibitory protein homologs that
RT   function to inhibit apoptosis and/or bind tumor necrosis factor
RT   receptor-associated factors.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   STRUCTURE BY NMR OF 266-363.
RX   MEDLINE=99332054; PubMed=10404221;
RA   Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT   "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT   repeat.";
RL   Nat. Struct. Biol. 6:648-651(1999).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC       WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC       FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC       NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC       MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC       AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC       LEUKOCYTES.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/BIRC3ID239.html".
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L49431; AAC41942.1; -.
DR   EMBL; U45879; AAC50372.1; -.
DR   EMBL; U37547; AAC50508.1; -.
DR   EMBL; BC016174; AAH16174.1; -.
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DR   PDB; 1QBH; 20-OCT-99.
DR   Genew; HGNC:590; BIRC2.
DR   MIM; 601721; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT   REPEAT       46    113       BIR 1.
FT   REPEAT      184    250       BIR 2.
FT   REPEAT      269    336       BIR 3.
FT   DOMAIN      453    543       CARD.
FT   ZN_FING     571    606       RING-TYPE.
FT   CONFLICT    157    157       S -> P (IN REF. 2).
FT   CONFLICT    308    308       C -> G (IN REF. 2).
FT   CONFLICT    414    414       Q -> L (IN REF. 2).
FT   CONFLICT    514    514       L -> W (IN REF. 2).
SQ   SEQUENCE   618 AA;  69899 MW;  C1778D328063586D CRC64;

  Query Match             36.3%;  Score 458.5;  DB 1;  Length 618;
  Best Local Similarity   29.5%;  Pred. No. 1.9e-29;
  Matches  104;  Conservative   50;  Mismatches   82;  Indels  117;  Gaps    6;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  |  |||| |||| :|: | |:|| | |||  |:  :||| :
Db        266 MQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVE 325

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
              ||||:| |::|:  || |::: |     ||   |      | ::          |  :
Db        326 HAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSS 385

Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
                :   |::: |: |||:   ||: :: :| |:| ||||:  :|: |::|: :  | |
Db        386 EDAVMMNTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEE 445

Qy        165 ----------------------------------------------------LNQTSLQ 171
                                                                   |  ||
Db        446 KEKQAEEMASDDLSLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQ 505

Qy        172 -RE-------------------------------------------------ISPEEPLRRL 183
               ||                                                 :| || ||||
Db        506 ARELIDTILVKGNAAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRL 565

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||: ||:|||: ::|||||||||| |::|| :: :|||:|  :|    | |:|
Db        566 QEERTCKVCMDKEVSVVFIPCGHLVVCQECAPSLRKCPICRGIIKGTVRTFLS 618


RESULT 9
BIR2_MOUSE
ID   BIR2_MOUSE     STANDARD;      PRT;   600 AA.
AC   O08863;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE   protein 1) (MIAP1) (MIAP-1).
GN   BIRC2 OR API1 OR IAP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=98110590; PubMed=9441758;
RA   Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT   "Genomic characterization of the mouse inhibitor of apoptosis protein
RT   1 and 2 genes.";
RL   Genomics 46:495-503(1997).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC       WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC       FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC       NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U88908; AAC53531.1; -.
DR   HSSP; Q13490; 1QBH.
DR   MGD; MGI:1197007; Birc2.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT       27     94       BIR 1.
FT   REPEAT      167    233       BIR 2.
FT   REPEAT      253    320       BIR 3.
FT   DOMAIN      436    525       CARD.
FT   ZN_FING     553    588       RING-TYPE.
SQ   SEQUENCE   600 AA;  67198 MW;  AD7F73E6849317D1 CRC64;

  Query Match             36.0%;  Score 455.5;  DB 1;  Length 600;
  Best Local Similarity   28.9%;  Pred. No. 3.2e-29;
  Matches  103;  Conservative   48;  Mismatches   80;  Indels  125;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  |: ::|| ||||  |  | |:|| | |||  |:  :||| :
Db        250 MQTHAARIRTFSNWPSSALVHSQELASAGFYYTGHSDDVKCFCCDGGLRCWESGDDPWVE 309

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSL------------EGALVQTTKKTPSL 101
              ||||:| |:|||  || |::: :     ||   |            : |:|       |
Db        310 HAKWFPRCEYLLRIKGQEFVSQVQAGYPHLLEQLLSTSDSPEDENADAAIVHFGPGESS- 368

Qy        102 TKRISDTI-FPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDT 160
                  | :    |::: |: |||    |:: :: :|  :| ||:|:  ||  |: |: : :
Db        369 ----EDVVMMSTPVVKAALEMGFSRSLVRQTVQRQILATGENYRTVSDLVIGLLDAEDEM 424

Qy        161 TENELNQ---------------------------------------------------- 167
               | :: |
Db        425 REEQMEQAAEEEESDDLALIRKNKMVLFQHLTCVTPMLYCLLSARAITEQECNAVKQKPH 484

Qy        168 -------------------TSLQ---REISP-------------------------EEPL 180
```

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                                  || :   ||| |                          || |
Db        485 TLQASTLIDTVLAKGNTAATSFRNSLREIDPALYRDIFVQQDIRSLPTDDIAALPMEEQL 544

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |:||||::||:|||| :::|||||||||| || || :: :|||:|   |    | |:|
Db        545 RKLQEERMCKVCMDREVSIVFIPCGHLVVCKDCAPSLRKCPICRGTIKGTVRTFLS 600


RESULT 10
BIR_CHICK
ID   BIR_CHICK      STANDARD;      PRT;   611 AA.
AC   Q90660;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE   protein).
GN   ITA.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=97101112; PubMed=8945639;
RA   Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT   "ITA, a vertebrate homologue of IAP that is expressed in T
RT   lymphocytes.";
RL   DNA Cell Biol. 15:981-988(1996).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC   -!- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC       BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC   -!- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC       T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U27466; AAB48118.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT   REPEAT       30     97       BIR 1.
FT   REPEAT      176    242       BIR 2.
FT   REPEAT      262    329       BIR 3.
FT   DOMAIN      446    536       CARD.
FT   ZN_FING     564    599       RING-TYPE.
SQ   SEQUENCE   611 AA;  69009 MW;  53FC9136F34EBDDD CRC64;
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  Query Match           36.0%;  Score 454.5;  DB 1;  Length 611;
  Best Local Similarity  29.1%;  Pred. No. 3.9e-29;
  Matches  105;  Conservative   52;  Mismatches   71;  Indels  133;  Gaps    9;

Qy          1 MTGYEARLITFGTW--MYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  :|||: ||  |     |  |||| |||| :|: | |:|| | |||  |:  :||| :
Db        259 MQTHEARVKTFINWPTRIPVQPEQLADAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWIE 318

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKK---------------- 97
              ||||:| |:|||  || |::: :     ||   |  :   |: |
Db        319 HAKWFPRCEYLLRVKGGEFVSQVQARFPHL---LWNSSCTTSDKPVDENMDPIIHFEPGE 375

Qy         98 TPSLTKRISDTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSA 156
              :||      | |  | |::: |: |||  : :|: :: :|  :  ||||:  ||::|::|
Db        376 SPS-----EDAIMMNTPVVKAALEMGFSRRLIKQTVQSKILATEENYKTVNDLVSELLTA 430

Qy        157 QKDTTENELNQ----------------------------------------TSLQREI-- 174
              : :  | |  :                                        | |: ::
Db        431 EDEKREEEKERQFEEVASDDLSLIRKNRMALFQRLTSVLPILGSLLSAKVITELEHDVIK 490

Qy        175 ----SP---------------------------------------------------- 176
                 :|
Db        491 QTTQTPSQARELIDTVLVKGNAAASIFRNCLKDFDPVLYKDLFVEKSMKYVPTEDVSGLP 550

Qy        177 -EEPLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFM 235
               || ||||||: ||:|||: :::|||||||||| ||:|| :: :||:|   |    | |:
Db        551 MEEQLRRLQEERTCKVCMDKEVSIVFIPCGHLVVCKECAPSLRKCPICRGTIKGTVRTFL 610

Qy        236 S 236
              |
Db        611 S 611


RESULT 11
BIR3_MOUSE
ID   BIR3_MOUSE     STANDARD;      PRT;   612 AA.
AC   Q62210; O08864;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
DE   protein 2) (MIAP2) (MIAP-2).
GN   BIRC3 OR API2 OR IAP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=96128127; PubMed=8548810;
RA   Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT   "The TNFR2-TRAF signaling complex contains two novel proteins related
RT   to baculoviral inhibitor of apoptosis proteins.";
RL   Cell 83:1243-1252(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=98110590; PubMed=9441758;
RA   Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT   "Genomic characterization of the mouse inhibitor of apoptosis protein
RT   1 and 2 genes.";
RL   Genomics 46:495-503(1997).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC       WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC       FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC       NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC   -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC       inhibit apoptotic suppressor activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC       LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
```

```
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L49433; AAC42078.1; -.
DR   EMBL; U88909; AAC53532.1; -.
DR   HSSP; Q13490; 1QBH.
DR   MGD; MGI:1197009; Birc3.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT       46    113       BIR 1.
FT   REPEAT      177    243       BIR 2.
FT   REPEAT      262    329       BIR 3.
FT   DOMAIN      447    537       CARD.
FT   ZN_FING     565    600       RING-TYPE.
FT   CONFLICT    380    380       E -> K (IN REF. 2).
SQ   SEQUENCE   612 AA;  69676 MW;  E08969D93C6C610D CRC64;

  Query Match            35.0%;  Score 443;  DB 1;  Length 612;
  Best Local Similarity  28.8%;  Pred. No. 3.3e-28;
  Matches  104;  Conservative   49;  Mismatches   76;  Indels  132;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||| ||  |  |  |  |||| |||| : : | |:|| | |||  |:| :||| :
Db        259 MQTHSARLRTFLYWPPSVPVQPEQLASAGFYYVDRNDDVKCFCCDGGLRCWEPGDDPWIE 318

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRISD------ 107
              ||||:| |::|:  || |::: |     ||   |      :|  ||   :  :|
Db        319 HAKWFPRCEFLIRMKGQEFVDEIQARYPHLLEQL-----LSTSDTPG--EENADPTETVV 371

Qy        108 -----------TIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSA 156
                        :   |::: |: |||    |:: :: :|  :| ||:|:  :|: |::|
Db        372 HFGPGESSEDVVMMSTPVVKAALEMGFSRSLVRQTVQRQILATGENYRTVNDIVSVLLNA 431

Qy        157 QKDTTENE---------------------------------------------------- 164
              : :  | |
Db        432 EDERREEEKERQTEEMASGDLSLIRKNRMALFQQLTHVLPILDNLLEASVITKQEHDIIR 491

Qy        165 -LNQTSLQ-RE----------------------------------------------IS 175
               |  || ||                                              :|
Db        492 QKTQIPLQARELIDTVLVKGNAAANIFKNSLKEIDSTLYENLFVEKNMKYIPTEDVSGLS 551

Qy        176 PEEPLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFM 235
               || |||||||: ||:|||| :::|||||||||| |::|| :: :||:|   |    | |:
Db        552 LEEQLRRLQEERTCKVCMDREVSIVFIPCGHLVVCQECAPSLRKCPICRGTIKGTVRTFL 611

Qy        236 S 236
              |
Db        612 S 612


RESULT 12
PIAP_PIG
ID   PIAP_PIG       STANDARD;      PRT;   358 AA.
AC   O62640;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative inhibitor of apoptosis.
GN   PIAP.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98162622; PubMed=9501011;
RA   Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT   "Cytokine induced expression of porcine inhibitor of apoptosis
RT   protein (iap) family member is regulated by NF-kappa B.";
RL   Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U79142; AAC39171.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00653; BIR; 2.
DR   SMART; SM00238; BIR; 2.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 2.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT        4     70       BIR 1.
FT   REPEAT       90    157       BIR 2.
FT   DOMAIN      193    283       CARD.
FT   ZN_FING     311    346       RING-TYPE.
SQ   SEQUENCE   358 AA;  40977 MW;  EB2268FA9A6190A4 CRC64;

  Query Match            33.8%;  Score 427;  DB 1;  Length 358;
  Best Local Similarity  34.3%;  Pred. No. 3.3e-27;
  Matches   96;  Conservative   45;  Mismatches   87;  Indels   52;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  | ||  ||  |  |  |: |||| |||| :|  | |:|| | |||  |:  :||| :
Db         87 MQTYAARFKTFCNWPSSIPVHPEQLASAGFYYMGHSDDVKCFCCDGGLRCWESGDDPWVE 146

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTP-----------SLT 102
              ||||:| |:||:  || |:|: :     ||   |      :|   |           ||
Db        147 HAKWFPRCEYLIRIKGQEFISRVQASYPHLLEQL-----LSTSDNPEDENAEPPNDLSLI 201

Qy        103 KRISDTIFPN-----PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQ 157
              ::    :| :     |:|   :  .  :    ::::: |||    : ::::   ||
Db        202 RKNRMALFQHLTCVLPILDSLLIARVISEQEHDVIKQKTQTSLQARELIDII---LVKGN 258

Qy        158 KDTT--ENELNQ-------------------TSLQREISPEEPLRRLQEEKLCKICMDRY 196
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              |  :| | :                    |    ::| || |||||||: ||:|||:
Db        259 YAATIFKNSLQEIDPMLYKHLFVQQDIKYIPTENVSDLSMEEQLRRLQEERTCKVCMDKE 318

Qy        197 IAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              :::|||||||||| || || :: :|||:|   |     | |:|
Db        319 VSIVFIPCGHLVVCKDCAPSLRKCPICRGTIKGTVRTFLS 358


RESULT 13
IAP2_DROME
ID   IAP2_DROME     STANDARD;      PRT;   498 AA.
AC   Q24307; Q24177; Q24115; Q24149; Q9V7G1;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Apoptosis 2 inhibitor (Inhibitor of apoptosis 2) (DIAP2) (DIAP) (IAP
DE   homolog A) (IAP-like protein) (DILP).
GN   IAP2 OR ILP OR DIHA OR CG8293.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye imaginal disk;
RX   MEDLINE=96128128; PubMed=8548811;
RA   Hay B.A., Wassarman D.A., Rubin G.M.;
RT   "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
RT   function to block cell death.";
RL   Cell 83:1253-1262(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=96149249; PubMed=8552191;
RA   Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA   Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT   "Suppression of apoptosis in mammalian cells by NAIP and a related
RT   family of IAP genes.";
RL   Nature 379:349-353(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Canton-S;
RX   MEDLINE=96256286; PubMed=8654366;
RA   Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA   Gilfillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;
RT   "A conserved family of cellular genes related to the baculovirus iap
RT   gene and encoding apoptosis inhibitors.";
RL   EMBO J. 15:2685-2694(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Canton-S;
RA   Ross J.L.;
RL   Thesis (1991), Vanderbilt University / Nashville, U.S.A.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [6]
RP   SEQUENCE OF 17-498 FROM N.A.
RC   TISSUE=Larva;
RX   MEDLINE=96209843; PubMed=8643514;
RA   Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT   "Cloning and expression of apoptosis inhibitory protein homologs that
RT   function to inhibit apoptosis and/or bind tumor necrosis factor
RT   receptor-associated factors.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC       HID-DEPENDENT CELL DEATH IN THE EYE.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT
CC       DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; L49441; AAC41610.1; -.
DR   EMBL; U45881; AAC46988.1; -.
DR   EMBL; U32373; AAC47155.1; -.
DR   EMBL; M96581; -; NOT_ANNOTATED_CDS.
DR   EMBL; AE003809; AAF58095.1; -.
DR   EMBL; U38809; AAB08398.1; -.
DR   HSSP; Q13490; 1QBH.
DR   FlyBase; FBgn0015247; Iap2.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00653; BIR; 3.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT        9     76       BIR 1.
FT   REPEAT      113    179       BIR 2.
FT   REPEAT      212    279       BIR 3.
FT   ZN_FING     451    486       RING-TYPE.
FT   CONFLICT      5      5       G -> V (IN REF. 2).
FT   CONFLICT     40     40       N -> K (IN REF. 2).
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FT   CONFLICT     64     65       ER -> AG (IN REF. 3).
FT   CONFLICT     94     94       E -> K (IN REF. 1).
FT   CONFLICT    282    282       A -> D (IN REF. 6).
FT   CONFLICT    286    286       A -> S (IN REF. 3).
FT   CONFLICT    302    302       P -> Q (IN REF. 2 AND 5).
FT   CONFLICT    303    303       P -> T (IN REF. 6).
FT   CONFLICT    327    327       A -> T (IN REF. 2).
FT   CONFLICT    369    376       ALEVREPP -> DWRCASR (IN REF. 3).
SQ   SEQUENCE   498 AA;  54506 MW;  66EC36DA6ED24AD6 CRC64;

  Query Match             31.7%;  Score 401;  DB 1;  Length 498;
  Best Local Similarity   30.8%;  Pred. No. 6e-25;
  Matches   89;  Conservative   46;  Mismatches   94;  Indels   60;  Gaps    4;

Qy          5 EARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKW 62
              :||| ||  |  |       ||:|| |     |:|:|||| || :|: :::|| :|||| 
Db        213 DARLRTFTDWPISNIQPASALAQAGLYYQKIGDQVRCFHCNIGLRSWQKEDEPWFEHAKW 272

Qy         63 YPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMG 122
               | |:::|  ||  |:: :  | :   :    |   |:|    :| :      :||: :| 
Db        273 SPKCQFVLLAKGPAYVSEVLATTAANASSPPATAPAPTLQ---ADVLMDEAPAKEALALG 329

Qy        123 FDFKDVKKIMEERIQTSGSNYKTLEVL------------------------------- 149
               |   |:  :: :: :||  : ||: |
Db        330 IDGGVVRNAIQRKLLSSGCAFSTLDELLHDIFDDAGAGAALEVREPPEPSAPFIEPCQAT 389

Qy        150 ----------VADLVSAQKDTTENELNQTSLQREI------------SPEEPLRRLQEEK 187
                       ||| : |:    |   | : :  ||            | ||  |:|:: :
Db        390 TSKAASVPIPVADSIPAKPQAAEAVANISKITDEIQKMSVATPNGNLSLEEENRQLKDAR 449

Qy        188 LCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||:|:|  : |||:||||| || ||| :|  |||| | |    | |:|
Db        450 LCKVCLDEEVGVVFLPCGHLATCNQCAPSVANCPMCRADIKGFVRTFLS 498


RESULT 14
BIR7_HUMAN
ID   BIR7_HUMAN     STANDARD;      PRT;   298 AA.
AC   Q96CA5; Q9H2A8; Q9HAP7; Q9BQV0;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of
DE   apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein)
DE   (ML-IAP) (Livin).
GN   BIRC7 OR KIAP OR MLIAP OR LIVIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Fetal kidney;
RX   PubMed=11162435;
RA   Lin J.-H., Deng G., Huang Q., Morser J.;
RT   "KIAP, a novel member of the inhibitor of apoptosis protein family.";
RL   Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Melanoma;
RX   PubMed=11322947;
RA   Ashhab Y., Alian A., Polliack A., Panet A., Yehuda D.B.;
RT   "Two splicing variants of a new inhibitor of apoptosis gene with
RT   different biological properties and tissue distribution pattern.";
RL   FEBS Lett. 495:56-60(2001).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Kidney;
RX   PubMed=11024045;
RA   Kasof G.M., Gomes B.C.;
RT   "Livin, a novel inhibitor of apoptosis protein family member.";
RL   J. Biol. Chem. 276:3238-3246(2001).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Skin;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND
RP   ASP-138.
RX   PubMed=11084335;
RA   Vucic D., Stennicke H.R., Pisabarro M.T., Salvesen G.S., Dixit V.M.;
RT   "ML-IAP, a novel inhibitor of apoptosis that is preferentially
RT   expressed in human melanomas.";
RL   Curr. Biol. 10:1359-1366(2000).
RN   [7]
RP   INTERACTION WITH SMAC.
RX   PubMed=11801603;
RA   Vucic D., Deshayes K., Ackerly H., Pisabarro M.T., Kadkhodayan S.,
RA   Fairbrother W.J., Dixit V.M.;
RT   "SMAC negatively regulates the anti-apoptotic activity of melanoma
RT   inhibitor of apoptosis (ML-IAP).";
RL   J. Biol. Chem. 277:12275-12279(2002).
RN   [8]
RP   ACTIVATION OF MAP KINASES.
RX   PubMed=11865055;
RA   Sanna M.G., da Silva Correia J., Ducrey O., Lee J., Nomoto K.,
RA   Schrantz N., Deveraux Q.L., Ulevitch R.J.;
RT   "IAP suppression of apoptosis involves distinct mechanisms: the
RT   TAK1/JNK1 signaling cascade and caspase inhibition.";
RL   Mol. Cell. Biol. 22:1754-1766(2002).
CC   -!- FUNCTION: Protects against apoptosis induced by TNF or by chemical
CC       agents such as adriamycin, etoposide or staurosporine. Suppression
CC       of apoptosis is mediated by activation of MAPK8/JNK1, and possibly
CC       also of MAPK9/JNK2. This activation depends on TAB1 and
CC       NR2C2/TAK1. In vitro, inhibits caspase-3 and proteolytic
CC       activation of pro-caspase-9. Isoform 1 blocks staurosporine-
CC       induced apoptosis and isoform 2 blocks etoposide-induced
CC       apoptosis.
CC   -!- SUBUNIT: Binds to caspase-9. Interaction with SMAC via the BIR
CC       domain disrupts binding to caspase-9 and apoptotic suppressor
CC       activity. Interacts with TAB1. In vitro, interacts with caspase-3
CC       and caspase-7 via its BIR domain.
CC   -!- SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern
CC       throughout the cytoplasm.
CC   -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1/Livin beta, 2/Livin alpha
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CC       (shown here) and 3; are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Very low levels or not detectable in most
CC       adult tissues. Detected in adult heart, placenta, lung, lymph
CC       node, spleen and ovary, and in several carcinoma cell lines
CC       (isoforms 1 and 2). Isoform 2 (but not isoform 1) is detected in
CC       fetal kidney, heart and spleen, and at lower levels in adult
CC       brain, skeletal muscle and peripheral blood leukocytes.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF301009; AAG37878.1; -.
DR   EMBL; AJ309298; CAC37337.1; -.
DR   EMBL; AJ309298; CAC37338.1; -.
DR   EMBL; AF311388; AAG33622.1; -.
DR   EMBL; AL121827; CAC36111.1; -.
DR   EMBL; AL121827; CAC36112.1; -.
DR   EMBL; AL121827; CAC36113.1; ALT_INIT.
DR   EMBL; BC014475; AAH14475.1; -.
DR   HSSP; Q13490; 1QBH.
DR   Genew; HGNC:13702; BIRC7.
DR   MIM; 605737; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Alternative splicing.
FT   REPEAT       90    155       BIR.
FT   ZN_FING     252    286       RING-TYPE.
FT   DOMAIN       64     69       POLY-GLU.
FT   VARSPLIC      1    149       MGPKDSAKCLHRGPQPSHWAAGDGPTQERCGPRSLGSPVLG
FT                                LDTCRAWDHVDGQILGQLRPLTEEEEEEGAGATLSRGPAFP
FT                                GMGSEELRLASFYDWPLTAEVPPELLAAAGFFHTGHQDKVR
FT                                CFFCYGGLQSWKRGDDPWTEHAKWFP -> MPLPWDYPEAP
FT                                WRRLHSSPPRPCPRALQGGGRRGPNPDPRGSKGLKQTVGAL
FT                                NPNLHLWGIC (IN ISOFORM 3).
FT   VARSPLIC    216    233       MISSING (IN ISOFORM 1).
FT   MUTAGEN      87     88       EE->AA: NO CHANGE IN SMAC INTERACTION AND
FT                                ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN     120    120       D->A: ABOLISHES INHIBITION OF CASPASES,
FT                                SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN     124    124       C->A: ABOLISHES INHIBITION OF CASPASES
FT                                AND ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN     138    138       D->A: ABOLISHES INHIBITION OF CASPASES,
FT                                SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
FT   CONFLICT    223    223       E -> Q (IN REF. 5).
SQ   SEQUENCE   298 AA;  32798 MW;  B2EAAEE531BEC101 CRC64;

  Query Match           29.5%;  Score 373.5;  DB 1;  Length 298;
  Best Local Similarity  32.2%;  Pred. No. 5.3e-23;
  Matches   82;  Conservative   42;  Mismatches   72;  Indels   59;  Gaps    9;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |   | || :|  |  :  |  | || |||:  | :|||:|| | ||| :||  :||| :
Db         84 MGSEELRLASFYDWPLTAEVPPELLAAAGFFHTGHQDKVRCFFCYGGLQSWKRGDDPWTE 143

Qy         59 HAKWYPGCKYLLEEKGHEYINNIHLTRS-LEGALVQTTKKTPSLTKRISDTI-------F 110
              ||||:| |::||  || ::::::  | | | |:      : |     :: ::
Db        144 HAKWFPSCQFLLRSKGRDFVHSVQETHSQLLGS--WDPWEEPEDAAPVAPSVPASGYPEL 201

Qy        111 PNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSL 170
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              | |               :::  |  |  |                          ::
Db        202 PTPR-------------REVQSESAQEPGG----------------------VSPAEA 224

Qy        171 QRE---ISP------EEPLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCP 221
              ||    : |      |  ||||||: ||:|:|| :::||:|||||| | :||  :  ||
Db        225 QRAWWVLEPPGARDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLV-CAECAPGLQLCP 283

Qy        222 MCSAVIDFKQRVFMS 236
              :| | :  : | |:|
Db        284 ICRAPVRSRVRTFLS 298


RESULT 15
IAP1_DROME
ID   IAP1_DROME     STANDARD;      PRT;   438 AA.
AC   Q24306;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis 1 inhibitor (Inhibitor of apoptosis 1) (DIAP1) (Thread
DE   protein).
GN   IAP1 OR TH.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye imaginal disk;
RX   MEDLINE=96128128; PubMed=8548811;
RA   Hay B.A., Wassarman D.A., Rubin G.M.;
RT   "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
RT   function to block cell death.";
RL   Cell 83:1253-1262(1995).
CC   -!- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC       HID-DEPENDENT CELL DEATH IN THE EYE.
CC   -!- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L49440; AAC41609.1; -.
DR   HSSP; Q13490; 1QBH.
DR   FlyBase; FBgn0003691; th.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00653; BIR; 2.
DR   SMART; SM00238; BIR; 2.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 2.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT       44    110       BIR 1.
FT   REPEAT      226    293       BIR 2.
FT   ZN_FING     391    426       RING-TYPE.
SQ   SEQUENCE   438 AA;  48098 MW;  A6C22C8EDF5AEF29 CRC64;

  Query Match           26.5%;  Score 335;  DB 1;  Length 438;
  Best Local Similarity  32.2%;  Pred. No. 1e-19;
  Matches   77;  Conservative   35;  Mismatches   91;  Indels   36;  Gaps    4;

Qy          6 ARLITFGTWMYSVNKE--QLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKWY 63
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                ||| ||  |  :: ::  ||| |||:  |  |:|:|| ||||| :|   ::||||||  |
Db        228 ARLRTFEAWPRNLKQKPHQLAEAGFFYTGVGDRVRCFSCGGGLMDWNDNDEPWEQHALWL 287

Qy         64 PGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPML----QEAI 119
               |:::   ||  ||                              ||:   |:|    :|:
Db        288 SQCRFVKLMKGQLYI---------------------------DTVAAKPVLAEEKEEST 319

Qy        120 RMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTT--ENELNQTSLQREISPE 177
                :| |     :  ||  ||| |: : :   ||  |:    |      :  |::    :
Db        320 SIGGDTVASTQASEEEQQTSLSSEEAVSGDVAPSVAPTAATRIFNKIVEATAVATPSTNS 379

Qy        178 EPLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
                : ||||||||        |:||||:| | :|| :| :||:|        ||: |
Db        380 SGSTSIPEEKLCKICYGAEYNTAFLPCGHVVACAKCASSVTKCPLCRKPFTDVMRVYFS 438

Search completed: June 19, 2003, 10:07:37
Job time : 25 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 19, 2003, 10:09:39 ; Search time 252 Seconds
(without alignments)
101.337 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264
Sequence: 1 MTGYEARLITFGTWMYSVNK.....VDRCPMCSAVIDFKQRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1052	83.2	278	9	US-09-964-899-39	Sequence 39, Appl
2	1052	83.2	497	9	US-09-201-936-4	Sequence 4, Appli
3	1052	83.2	497	10	US-09-974-592-4	Sequence 4, Appli
4	989	78.2	496	9	US-09-201-936-10	Sequence 10, Appl
5	989	78.2	496	10	US-09-974-592-10	Sequence 10, Appl
6	466.5	36.9	604	9	US-09-201-936-6	Sequence 6, Appli
7	466.5	36.9	604	10	US-09-974-592-6	Sequence 6, Appli
8	458.5	36.3	438	1	US-08-464-588-2	Sequence 2, Appli
9	458.5	36.3	438	9	US-10-323-643-2	Sequence 2, Appli
10	458.5	36.3	618	9	US-10-153-668-338	Sequence 338, App
11	455.5	36.0	600	10	US-09-974-592-12	Sequence 12, Appl
12	454.5	36.0	618	9	US-09-201-936-8	Sequence 8, Appli
13	454.5	36.0	618	10	US-09-974-592-8	Sequence 8, Appli
14	453	35.8	107	9	US-09-965-967-20	Sequence 20, Appl
15	443	35.0	612	10	US-09-974-592-14	Sequence 14, Appl
16	437	34.6	591	9	US-09-201-936-42	Sequence 42, Appl
17	433.5	34.3	602	9	US-09-201-936-40	Sequence 40, Appl
18	400	31.6	498	9	US-09-201-936-13	Sequence 13, Appl
19	376.5	29.8	280	9	US-10-244-586-3	Sequence 3, Appli
20	373.5	29.5	298	9	US-10-235-026-2	Sequence 2, Appli
21	347	27.5	66	9	US-09-201-936-25	Sequence 25, Appl
22	334	26.4	66	9	US-09-201-936-24	Sequence 24, Appl
23	320	25.3	346	9	US-10-041-859-2	Sequence 2, Appli
24	314.5	24.9	275	9	US-09-201-936-12	Sequence 12, Appl
25	314.5	24.9	275	9	US-10-323-643-9	Sequence 9, Appli
26	312.5	24.7	268	9	US-10-323-643-10	Sequence 10, Appl
27	262	20.7	50	9	US-10-138-618-28	Sequence 28, Appl
28	262	20.7	50	9	US-10-138-618-29	Sequence 29, Appl
29	262	20.7	50	9	US-10-138-618-32	Sequence 32, Appl
30	248	19.6	172	9	US-10-041-859-12	Sequence 12, Appl
31	247	19.5	172	9	US-10-041-859-8	Sequence 8, Appli
32	242	19.1	172	9	US-10-041-859-10	Sequence 10, Appl
33	241	19.1	172	9	US-10-041-859-9	Sequence 9, Appli
34	237	18.8	46	9	US-09-201-936-35	Sequence 35, Appl
35	237	18.8	172	9	US-10-041-859-11	Sequence 11, Appl
36	235	18.6	48	10	US-09-864-761-46539	Sequence 46539, A
37	234	18.5	172	9	US-10-041-859-13	Sequence 13, Appl
38	220	17.4	46	9	US-09-201-936-34	Sequence 34, Appl
39	209.5	16.6	1403	8	US-08-913-322-22	Sequence 22, Appl
40	209.5	16.6	1403	8	US-08-913-322-24	Sequence 24, Appl
41	209.5	16.6	1403	9	US-10-285-408-1	Sequence 1, Appli
42	208	16.5	68	9	US-09-201-936-26	Sequence 26, Appl
43	198	15.7	109	9	US-09-965-967-30	Sequence 30, Appl
44	197	15.6	50	9	US-10-138-618-21	Sequence 21, Appl
45	197	15.6	68	9	US-09-201-936-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

Query Match 83.2%; Score 1052; DB 9; Length 278;
Best Local Similarity 80.1%; Pred. No. 1.6e-92;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

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Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:|||||||||||||||:|: |||:|||||||| :||| ||||||||
Db         43 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 102

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
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Db        103 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 162

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:||||||||:|||| ::| :|||||:||| || |
Db        163 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 222

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||::|||
Db        223 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 278
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RESULT 2
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G.
;  APPLICANT: MacKenzie, Alexander E.
;  APPLICANT: Baird, Stephen
;  APPLICANT: Liston, Peter
;  TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;  TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;  FILE REFERENCE: 07891/003003
;  CURRENT APPLICATION NUMBER: US/09/201,936
;  CURRENT FILING DATE: 1998-12-01
;  EARLIER APPLICATION NUMBER: 09/011,356
;  EARLIER FILING DATE: 1998-02-04
;  EARLIER APPLICATION NUMBER: PCT/IB96/01022
;  EARLIER FILING DATE: 1996-08-05
;  EARLIER APPLICATION NUMBER: 08/576,956
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 08/511,485
;  EARLIER FILING DATE: 1995-08-04
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-201-936-4

  Query Match             83.2%;  Score 1052;  DB 9;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 3.6e-92;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: ||||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
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Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
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Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 3
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009004
;  CURRENT APPLICATION NUMBER: US/09/974,592
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: US 09/617,053
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-974-592-4

  Query Match             83.2%;  Score 1052;  DB 10;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 3.6e-92;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
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Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:|||||||||:|||| ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 4
US-09-201-936-10
; Sequence 10, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G.
;  APPLICANT: MacKenzie, Alexander E.
;  APPLICANT: Baird, Stephen
;  APPLICANT: Liston, Peter
;  TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;  TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;  FILE REFERENCE: 07891/003003
;  CURRENT APPLICATION NUMBER: US/09/201,936
;  CURRENT FILING DATE: 1998-12-01
;  EARLIER APPLICATION NUMBER: 09/011,356
;  EARLIER FILING DATE: 1998-02-04
;  EARLIER APPLICATION NUMBER: PCT/IB96/01022
;  EARLIER FILING DATE: 1996-08-05
;  EARLIER APPLICATION NUMBER: 08/576,956
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 08/511,485
;  EARLIER FILING DATE: 1995-08-04
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-201-936-10

  Query Match             78.2%;  Score 989;  DB 9;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 3.8e-86;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
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Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
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Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
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              ||| |||:|| |||:|||||||:| :||||:|||||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| ||||||||||:|||| || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 5
US-09-974-592-10
; Sequence 10, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009004
;  CURRENT APPLICATION NUMBER: US/09/974,592
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: US 09/617,053
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-974-592-10

  Query Match             78.2%;  Score 989;  DB 10;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 3.8e-86;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||:|||||:||||||||||||||||:|: |||:|||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              | ||||||||:||| |||||||||  || :| :| :||| |||:| |||| |||:|||||
Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:||||||:| :||||:|||||||||| ||:| :||||||::|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| ||||||||||:|||| || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 6
US-09-201-936-6
; Sequence 6, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G.
;  APPLICANT: MacKenzie, Alexander E.
;  APPLICANT: Baird, Stephen
;  APPLICANT: Liston, Peter
;  TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;  TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;  FILE REFERENCE: 07891/003003
;  CURRENT APPLICATION NUMBER: US/09/201,936
;  CURRENT FILING DATE: 1998-12-01
;  EARLIER APPLICATION NUMBER: 09/011,356
;  EARLIER FILING DATE: 1998-02-04
;  EARLIER APPLICATION NUMBER: PCT/IB96/01022
;  EARLIER FILING DATE: 1996-08-05
;  EARLIER APPLICATION NUMBER: 08/576,956
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 08/511,485
;  EARLIER FILING DATE: 1995-08-04
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 604
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-201-936-6

  Query Match             36.9%;  Score 466.5;  DB 9;  Length 604;
  Best Local Similarity   30.7%;  Pred. No. 4.1e-36;
  Matches  110;  Conservative   40;  Mismatches   81;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||  ||  |  |  || |||| |||| :|  | |:|| | |||  |:  :||| |
Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106
              ||||:| |:||:  || |:|  :     ||   |      :|  :|      |
Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHLEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159
                   | |  | |::  |: |||    ||: :: :|  :| ||: :  || ||::|: :
Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN---------------------------------------------- 166
                      | | | |
Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ----------------------------------------------REISPEE 178
              |||||                                              ::  ||
Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546
                  *
Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||| ||: ||:||: :::|||||||| || || :: :||:| : |    | |:|
Db        547 QLRRLPEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604


RESULT 7
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009004
;  CURRENT APPLICATION NUMBER: US/09/974,592
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: US 09/617,053
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 604
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-974-592-6
```

```
  Query Match            36.9%;  Score 466.5;  DB 10;  Length 604;
  Best Local Similarity   30.7%;  Pred. No. 4.1e-36;
  Matches  110;  Conservative   40;  Mismatches   81;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||  ||  |  |  || |||| |||| :|  | |:|| | |||  |:  :||| |
Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106
              ||||:| |:||:  || |:|  :     ||   |      :|  :|      |
Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHLEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159
                   | |  | |::  |: |||    ||: :: :|  :| ||: :  || ||::|: :
Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN---------------------------------------------- 166
                      | | | |
Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ-------------------------------------------------REISPEE 178
              |||||                                                 ::  ||
Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||| ||: ||:|||: :::|||||||||| || || :: :|||:| : |    | |:|
Db        547 QLRRLPEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604
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RESULT 8
US-08-464-588-2
; Sequence 2, Application US/08464588
; Publication No. US20030073159A1
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,588
; FILING DATE: June.5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05922
; FILING DATE: 11 MAY 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-464-588-2

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  Query Match            36.3%;  Score 458.5;  DB 1;  Length 438;
  Best Local Similarity   29.5%;  Pred. No. 1.5e-35;
  Matches  104;  Conservative   50;  Mismatches   82;  Indels  117;  Gaps    6;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  | |||| |||| :|: | |:|| | |||  |:  :||| :
Db         86 MQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVE 145

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
              ||||:| |::|:  || |::: |      ||   |       | ::          |  :
Db        146 HAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSS 205

Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
                  :   |::: |: |||:   ||: :: :| |:| ||||:  :|: |::|: :  | |
Db        206 EDAVMMNTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEE 265

Qy        165 ----------------------------------------------------LNQTSLQ 171
                                                                   |  ||
Db        266 KEKQAEEMASDDLSLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQ 325

Qy        172 -RE-------------------------------------------------ISPEEPLRRL 183
               ||                                                :| || ||||
Db        326 ARELIDTILVKGNAAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRL 385

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||: ||:||: ::|||||||||| |::|| :: :||:|  :|    | |:|
Db        386 QEERTCKVCMDKEVSVVFIPCGHLVVCQECAPSLRKCPICRGIIKGTVRTFLS 438
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RESULT 9
US-10-323-643-2
; Sequence 2, Application US/10323643
; Publication No. US20030108552A1
; GENERAL INFORMATION:
; APPLICANT: He, et al.
; TITLE OF INVENTION: Human Inhibitor of Apotosis Gene 1
; FILE REFERENCE: PF165P1D1
; CURRENT APPLICATION NUMBER: US/10/323,643
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 08/464,588
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/05922
; PRIOR FILING DATE: 1995-05-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-643-2

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  Query Match            36.3%;  Score 458.5;  DB 9;  Length 438;
  Best Local Similarity   29.5%;  Pred. No. 1.5e-35;
  Matches  104;  Conservative   50;  Mismatches   82;  Indels  117;  Gaps    6;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  | |||| |||| :|: | |:|| | |||  |:  :||| :
Db         86 MQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVE 145

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
              ||||:| |::|:  || |::: |      ||   |       | ::          |  :
Db        146 HAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSS 205

Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
                  :   |::: |: |||:   ||: :: :| |:| ||||:  :|: |::|: :  | |
Db        206 EDAVMMNTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEE 265

Qy        165 ----------------------------------------------------LNQTSLQ 171
                                                                   |  ||
Db        266 KEKQAEEMASDDLSLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQ 325

Qy        172 -RE-------------------------------------------------ISPEEPLRRL 183
               ||                                                :| || ||||
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```
Db        326 ARELIDTILVKGNAAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRL 385

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||: ||:|||: ::|||||||||| |::|| :: :||:|  :|    | |:|
Db        386 QEERTCKVCMDKEVSVVFIPCGHLVVCQECAPSLRKCPICRGIIKGTVRTFLS 438


RESULT 10
US-10-153-668-338
; Sequence 338, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
;  APPLICANT: HONDA, Goichi
;  APPLICANT:  MATSUDA, Akio
;  APPLICANT:  MURAMATSU, Shuji
;  APPLICANT:  ISHIZAWA, Kenya
;  TITLE OF INVENTION: STAT6 Activating Gene
;  FILE REFERENCE: 1254-0207P
;  CURRENT APPLICATION NUMBER: US/10/153,668
;  CURRENT FILING DATE:  2002-05-24
;  PRIOR APPLICATION NUMBER: US 60/293,172
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/316,031
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 60/328,403
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: JP 2001-157043
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: JP 2001-260681
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: JP 2001-313175
;  PRIOR FILING DATE: 2001-10-10
;  NUMBER OF SEQ ID NOS: 488
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 338
;   LENGTH: 618
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-153-668-338

  Query Match             36.3%;  Score 458.5;  DB 9;  Length 618;
  Best Local Similarity   29.5%;  Pred. No. 2.5e-35;
  Matches  104;  Conservative   50;  Mismatches   82;  Indels  117;  Gaps    6;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  |  |||| |||| :|: | |:|| | |||  |:  :||| :
Db        266 MQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVE 325

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
              ||||:| |::|:  || |::: |     ||   |      | ::          |  :
Db        326 HAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSS 385

Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
                :   |::: |: |||:   ||: :: :| |:| ||||:  :|: |::|: :  | |
Db        386 EDAVMMNTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEE 445

Qy        165 ----------------------------------------------------LNQTSLQ 171
                                                                   |  ||
Db        446 KEKQAEEMASDDLSLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQ 505

Qy        172 -RE-----------------------------------------------ISPEEPLRRL 183
               ||                                               :| || ||||
Db        506 ARELIDTILVKGNAAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRL 565

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||: ||:|||: ::|||||||||| |::|| :: :||:|  :|    | |:|
Db        566 QEERTCKVCMDKEVSVVFIPCGHLVVCQECAPSLRKCPICRGIIKGTVRTFLS 618


RESULT 11
US-09-974-592-12
; Sequence 12, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009004
;  CURRENT APPLICATION NUMBER: US/09/974,592
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: US 09/617,053
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-974-592-12

  Query Match             36.0%;  Score 455.5;  DB 10;  Length 600;
  Best Local Similarity   28.9%;  Pred. No. 4.6e-35;
  Matches  103;  Conservative   48;  Mismatches   80;  Indels  125;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  |: ::|| ||||  |  | |:|| | |||  |:  :||| :
Db        250 MQTHAARIRTFSNWPSSALVHSQELASAGFYYTGHSDDVKCFCCDGGLRCWESGDDPWVE 309

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSL----------EGALVQTTKKTPSL 101
              ||||:| |:|||  || |::: :     ||   |          : |:|       |
Db        310 HAKWFPRCEYLLRIKGQEFVSQVQAGYPHLLEQLLSTSDSPEDENADAAIVHFGPGESS- 368

Qy        102 TKRISDTI-FPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDT 160
                  | :    |::: |: |||    |:: :: :|  :| ||:|:  ||  |: |: :
Db        369 ----EDVVMMSTPVVKAALEMGFSRSLVRQTVQRQILATGENYRTVSDLVIGLLDAEDEM 424

Qy        161 TENELNQ---------------------------------------------------- 167
                | :: |
Db        425 REEQMEQAAEEEESDDLALIRKNKMVLFQHLTCVTPMLYCLLSARAITEQECNAVKQKPH 484

Qy        168 -------------------TSLQ---REISP-------------------------EEPL 180
                                  || :   ||| |                        || |
Db        485 TLQASTLIDTVLAKGNTAATSFRNSLREIDPALYRDIFVQQDIRSLPTDDIAALPMEEQL 544

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |:||||::||:|||| :::|||||||||| || || :: :||:|   |    | |:|
Db        545 RKLQEERMCKVCMDREVSIVFIPCGHLVVCKDCAPSLRKCPICRGTIKGTVRTFLS 600


RESULT 12
US-09-201-936-8
; Sequence 8, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G.
;  APPLICANT: MacKenzie, Alexander E.
;  APPLICANT: Baird, Stephen
;  APPLICANT: Liston, Peter
;  TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;  TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;  FILE REFERENCE: 07891/003003
;  CURRENT APPLICATION NUMBER: US/09/201,936
;  CURRENT FILING DATE: 1998-12-01
;  EARLIER APPLICATION NUMBER: 09/011,356
;  EARLIER FILING DATE: 1998-02-04
;  EARLIER APPLICATION NUMBER: PCT/IB96/01022
;  EARLIER FILING DATE: 1996-08-05
;  EARLIER APPLICATION NUMBER: 08/576,956
```

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;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 08/511,485
;  EARLIER FILING DATE: 1995-08-04
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 618
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-201-936-8

  Query Match            36.0%;  Score 454.5;  DB 9;  Length 618;
  Best Local Similarity  29.5%;  Pred. No. 6e-35;
  Matches  104;  Conservative   49;  Mismatches   83;  Indels  117;  Gaps    6;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  |  |||| |||| :|: | |:|| | |||  |:  :||| :
Db        266 MQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVE 325

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
              ||||:| |::|:  || |::: |     ||   |      | ::          |  :
Db        326 HAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSS 385

Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
                :   |::: |: |||:   ||: :  :| |:| ||||:  :|: |::|: :  | |
Db        386 EDAVMMNTPVVKSALEMGFNRDLVKQTVLSKILTTGENYKTVNDIVSALLNAEDEKREEE 445

Qy        165 ----------------------------------------------------LNQTSLQ 171
                                                                   |  ||
Db        446 KEKQAEEMASDDLSLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQ 505

Qy        172 -RE-----------------------------------------------ISPEEPLRRL 183
               ||                                              :| || ||||
Db        506 ARELIDTIWVKGNAAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRL 565

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||: ||:||: ::|||||||||| |::|| :: :||:|  :|    | |:|
Db        566 QEERTCKVCMDKEVSVVFIPCGHLVVCQECAPSLRKCPICRGIIKGTVRTFLS 618


RESULT 13
US-09-974-592-8
; Sequence 8, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009004
;  CURRENT APPLICATION NUMBER: US/09/974,592
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: US 09/617,053
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 618
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-974-592-8

  Query Match            36.0%;  Score 454.5;  DB 10;  Length 618;
  Best Local Similarity  29.5%;  Pred. No. 6e-35;
  Matches  104;  Conservative   49;  Mismatches   83;  Indels  117;  Gaps    6;

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Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
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Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
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Db        386 EDAVMMNTPVVKSALEMGFNRDLVKQTVLSKILTTGENYKTVNDIVSALLNAEDEKREEE 445

Qy        165 ----------------------------------------------------LNQTSLQ 171
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Qy        172 -RE-----------------------------------------------ISPEEPLRRL 183
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Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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RESULT 14
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; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
;  APPLICANT: Shi, Yigong
;  TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
;  FILE REFERENCE: PU-0031 (01-1739-1)
;  CURRENT APPLICATION NUMBER: US/09/965,967
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/236,574
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/256,830
;  PRIOR FILING DATE: 2000-12-20
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-965-967-20

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RESULT 15
US-09-974-592-14
; Sequence 14, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
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;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009004
;  CURRENT APPLICATION NUMBER: US/09/974,592
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: US 09/617,053
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 612
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-974-592-14

  Query Match             35.0%;  Score 443;  DB 10;  Length 612;
  Best Local Similarity   28.8%;  Pred. No. 7.4e-34;
  Matches  104;  Conservative   49;  Mismatches   76;  Indels  132;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
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Db        259 MQTHSARLRTFLYWPPSVPVQPEQLASAGFYYVDRNDDVKCFCCDGGLRCWEPGDDPWIE 318

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRISD------ 107
              ||||:| |::|:  || |::: |     ||   |      :|  ||   :  :|
Db        319 HAKWFPRCEFLIRMKGQEFVDEIQARYPHLLEQL-----LSTSDTPG--EENADPTETVV 371

Qy        108 ----------TIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSA 156
                       :   |::: |: |||    |:: :: :|  :| ||:|:  :|: |::|
Db        372 HFGPGESSKDVVMMSTPVVKAALEMGFSRSLVRQTVQRQILATGENYRTVNDIVSVLLNA 431

Qy        157 QKDTTENE---------------------------------------------------- 164
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Db        432 EDERREEEKERQTEEMASGDLSLIRKNRMALFQQLTHVLPILDNLLEASVITKQEHDIIR 491

Qy        165 -LNQTSLQ-RE-----------------------------------------------IS 175
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Qy        176 PEEPLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFM 235
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Qy        236 S 236
              |
Db        612 S 612


Search completed: June 19, 2003, 10:26:01
Job time : 253 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:05 ; Search time 15 Seconds
(without alignments)
462.921 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264
Sequence: 1 MTGYEARLITFGTWMYSVNK.....VDRCPMCSAVIDFKQRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1264	100.0	236	4	US-09-121-979-4	Sequence 4, Appli
2	1264	100.0	236	4	US-09-332-319-4	Sequence 4, Appli
3	1264	100.0	236	4	US-09-239-867-2	Sequence 2, Appli
4	1052	83.2	236	4	US-09-239-867-4	Sequence 4, Appli
5	1052	83.2	497	2	US-08-511-485-4	Sequence 4, Appli
6	1052	83.2	497	3	US-09-212-971-4	Sequence 4, Appli
7	1052	83.2	497	4	US-08-800-929A-4	Sequence 4, Appli
8	1052	83.2	497	4	US-09-617-053A-4	Sequence 4, Appli
9	989	78.2	496	2	US-08-511-485-10	Sequence 10, Appl
10	989	78.2	496	3	US-09-212-971-10	Sequence 10, Appl
11	989	78.2	496	4	US-08-800-929A-10	Sequence 10, Appl
12	989	78.2	496	4	US-09-617-053A-10	Sequence 10, Appl
13	472.5	37.4	604	4	US-08-569-749-4	Sequence 4, Appli
14	472.5	37.4	604	5	PCT-US96-12860-4	Sequence 4, Appli
15	466.5	36.9	604	2	US-08-511-485-6	Sequence 6, Appli
16	466.5	36.9	604	3	US-09-212-971-6	Sequence 6, Appli
17	466.5	36.9	604	4	US-08-800-929A-6	Sequence 6, Appli
18	466.5	36.9	604	4	US-09-617-053A-6	Sequence 6, Appli
19	458.5	36.3	438	5	PCT-US95-05922A-2	Sequence 2, Appli
20	458.5	36.3	618	4	US-08-569-749-2	Sequence 2, Appli
21	458.5	36.3	618	4	US-09-069-023-29	Sequence 29, Appl
22	458.5	36.3	618	5	PCT-US96-12860-2	Sequence 2, Appli
23	455.5	36.0	600	3	US-09-212-971-12	Sequence 12, Appl
24	455.5	36.0	600	4	US-08-800-929A-12	Sequence 12, Appl
25	455.5	36.0	600	4	US-09-617-053A-12	Sequence 12, Appl
26	454.5	36.0	618	2	US-08-511-485-8	Sequence 8, Appli
27	454.5	36.0	618	3	US-09-212-971-8	Sequence 8, Appli
28	454.5	36.0	618	4	US-08-800-929A-8	Sequence 8, Appli
29	454.5	36.0	618	4	US-09-617-053A-8	Sequence 8, Appli
30	443	35.0	612	3	US-09-212-971-14	Sequence 14, Appl
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33	443	35.0	612	4	US-09-617-053A-14	Sequence 14, Appl
34	443	35.0	612	5	PCT-US96-12860-14	Sequence 14, Appl
35	400	31.6	498	2	US-08-511-485-13	Sequence 13, Appl
36	347	27.5	66	2	US-08-511-485-25	Sequence 25, Appl
37	334	26.4	66	2	US-08-511-485-24	Sequence 24, Appl
38	314.5	24.9	275	2	US-08-511-485-12	Sequence 12, Appl
39	314.5	24.9	275	3	US-08-836-134-21	Sequence 21, Appl
40	314.5	24.9	275	4	US-09-493-784-21	Sequence 21, Appl
41	312.5	24.7	268	3	US-08-836-134-22	Sequence 22, Appl
42	312.5	24.7	268	4	US-09-493-784-22	Sequence 22, Appl
43	262	20.7	50	4	US-08-975-080-28	Sequence 28, Appl
44	262	20.7	50	4	US-08-975-080-29	Sequence 29, Appl
45	262	20.7	50	4	US-08-975-080-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-121-979-4
; Sequence 4, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979.
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-979-4

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Best Local Similarity 100.0%; Pred. No. 2.6e-127;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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RESULT 2
US-09-332-319-4
; Sequence 4, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF

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;  FILE REFERENCE: 07891/021002
;  CURRENT APPLICATION NUMBER: US/09/332,319
;  CURRENT FILING DATE: 1999-06-14
;  EARLIER APPLICATION NUMBER: 09/121,979
;  EARLIER FILING DATE: 1998-07-24
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-332-319-4

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  Best Local Similarity  100.0%;  Pred. No. 2.6e-127;
  Matches  236;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
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Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
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Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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RESULT 3
US-09-239-867-2
; Sequence 2, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
;  APPLICANT:  Robert G. Korneluk et al.
;  TITLE OF INVENTION:  METHODS AND COMPOUNDS FOR MODULATING
;  TITLE OF INVENTION:  MALE FERTILITY
;  FILE REFERENCE:  07891/018002
;  CURRENT APPLICATION NUMBER: US/09/239,867
;  CURRENT FILING DATE:  1999-01-29
;  PRIOR APPLICATION NUMBER:  60/073,001
;  PRIOR FILING DATE:  1998-01-29
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-239-867-2

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  Best Local Similarity  100.0%;  Pred. No. 2.6e-127;
  Matches  236;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
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Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
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Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 4
US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
;  APPLICANT:  Robert G. Korneluk et al.
;  TITLE OF INVENTION:  METHODS AND COMPOUNDS FOR MODULATING
;  TITLE OF INVENTION:  MALE FERTILITY
;  FILE REFERENCE:  07891/018002
;  CURRENT APPLICATION NUMBER: US/09/239,867
;  CURRENT FILING DATE:  1999-01-29
;  PRIOR APPLICATION NUMBER:  60/073,001
;  PRIOR FILING DATE:  1998-01-29
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-239-867-4

  Query Match           83.2%;  Score 1052;  DB 4;  Length 236;
  Best Local Similarity  80.1%;  Pred. No. 1.3e-104;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

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Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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Db        181 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 236


RESULT 5
US-08-511-485-4
; Sequence 4, Application US/08511485
; Patent No. 5919912
;  GENERAL INFORMATION:
;    APPLICANT:  Korneluk, Robert G.
;    APPLICANT:  Mackenzie, Alexander E.
;    APPLICANT:  Baird, Stephen
;    TITLE OF INVENTION:  MAMMALIAN IAP GENE FAMILY, PRIMERS,
;    TITLE OF INVENTION:  PROBES, AND DETECTION METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/511,485
;      FILING DATE:  04-AUG-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
```

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;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  07540/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  497 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  both
;    MOLECULE TYPE:  protein
US-08-511-485-4

  Query Match             83.2%;  Score 1052;  DB 2;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 4e-104;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: ||||:|||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:|||||||||:||||: ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:||||||||||||||||:||||  || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 6
US-09-212-971-4
; Sequence 4, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT: MacKenzie, Alexander E
;  APPLICANT: Liston, Peter
;  APPLICANT: Baird, Stephen
;  APPLICANT: Tsang, Benjamin K
;  APPLICANT: Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION: DISEASE
;  FILE REFERENCE: 07891/009002
;  CURRENT APPLICATION NUMBER: US/09/212,971B
;  CURRENT FILING DATE: 1998-12-16
;  EARLIER APPLICATION NUMBER: 60/017,354
;  EARLIER FILING DATE: 1996-04-26
;  EARLIER APPLICATION NUMBER: 60/030,590
;  EARLIER FILING DATE: 1996-11-14
;  EARLIER APPLICATION NUMBER: 08/800,929
;  EARLIER FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-212-971-4

  Query Match             83.2%;  Score 1052;  DB 3;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 4e-104;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: ||||:|||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:|||||||||:||||: ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:||||||||||||||||:||||  || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 7
US-08-800-929A-4
; Sequence 4, Application US/08800929A
; Patent No. 6133437
;  GENERAL INFORMATION:
;    APPLICANT:  Korneluk, Robert G
;    APPLICANT:  MacKenzie, Alexander E
;    APPLICANT:  Liston, Peter
;    APPLICANT:  Baird, Stephen
;    APPLICANT:  Tsang, Benjamin K
;    APPLICANT:  Pratt, Christine
;    TITLE OF INVENTION:  DETECTION AND MODULATION OF
;    TITLE OF INVENTION:  IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
;    TITLE OF INVENTION:  DISEASE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/800,929A
;      FILING DATE:  13-FEB-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,590
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/017,354
;      FILING DATE:  26-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bieker-Brady, Kristina
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  07891/009001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  497 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-800-929A-4

  Query Match             83.2%;  Score 1052;  DB 4;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 4e-104;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;
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Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|||||:|| |||||:||||||||:|||: ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 8
US-09-617-053A-4
; Sequence 4, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009003
;  CURRENT APPLICATION NUMBER: US/09/617,053A
;  CURRENT FILING DATE:  2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-617-053A-4

  Query Match             83.2%;  Score 1052;  DB 4;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 4e-104;
  Matches  189;  Conservative   25;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|||||:|| |||||:||||||||:|||: ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 9
US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 5919912
;  GENERAL INFORMATION:
;    APPLICANT:  Korneluk, Robert G.
;    APPLICANT:  Mackenzie, Alexander E.
;    APPLICANT:  Baird, Stephen
;    TITLE OF INVENTION:  MAMMALIAN IAP GENE FAMILY, PRIMERS,
;    TITLE OF INVENTION:  PROBES, AND DETECTION METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/511,485
;      FILING DATE:  04-AUG-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  07540/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  both
;    MOLECULE TYPE:  protein
US-08-511-485-10

  Query Match             78.2%;  Score 989;  DB 2;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 2.2e-97;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              | |||||||:||| |||||||||  || :| :| :||| |||:| |||| |||:|||||
Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:|||||:| :|||||:|||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| ||||||||||:|||  || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 10
US-09-212-971-10
; Sequence 10, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT: MacKenzie, Alexander E
;  APPLICANT: Liston, Peter
;  APPLICANT: Baird, Stephen
;  APPLICANT: Tsang, Benjamin K
;  APPLICANT: Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION: DISEASE
;  FILE REFERENCE: 07891/009002
;  CURRENT APPLICATION NUMBER: US/09/212,971B
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;  CURRENT FILING DATE: 1998-12-16
;  EARLIER APPLICATION NUMBER: 60/017,354
;  EARLIER FILING DATE: 1996-04-26
;  EARLIER APPLICATION NUMBER: 60/030,590
;  EARLIER FILING DATE: 1996-11-14
;  EARLIER APPLICATION NUMBER: 08/800,929
;  EARLIER FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-212-971-10

  Query Match             78.2%;  Score 989;  DB 3;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 2.2e-97;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              | |||||||||:||| |||||||||  || :| :| :||| |||:| |||| |||:|||||
Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||·|||:|||||:| :||||:|||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| |||||||||:|||| || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 11
US-08-800-929A-10
; Sequence 10, Application US/08800929A
; Patent No. 6133437
;  GENERAL INFORMATION:
;    APPLICANT:  Korneluk, Robert G
;    APPLICANT:  MacKenzie, Alexander E
;    APPLICANT:  Liston, Peter
;    APPLICANT:  Baird, Stephen
;    APPLICANT:  Tsang, Benjamin K
;    APPLICANT:  Pratt, Christine
;    TITLE OF INVENTION:  DETECTION AND MODULATION OF
;    TITLE OF INVENTION:  IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;    TITLE OF INVENTION:  DISEASE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/800,929A
;      FILING DATE:  13-FEB-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,590
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/017,354
;      FILING DATE:  26-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bieker-Brady, Kristina
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  07891/009001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-800-929A-10

  Query Match             78.2%;  Score 989;  DB 4;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 2.2e-97;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              | |||||||||:||| |||||||||  || :| :| :||| |||:| |||| |||:|||||
Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:|||||:| :||||:|||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| |||||||||:|||| || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 12
US-09-617-053A-10
; Sequence 10, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009003
;  CURRENT APPLICATION NUMBER: US/09/617,053A
;  CURRENT FILING DATE:  2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-617-053A-10

  Query Match             78.2%;  Score 989;  DB 4;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 2.2e-97;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
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Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236

Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 13
US-08-569-749-4
; Sequence 4, Application US/08569749
; Patent No. 6187557
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Goeddel, David V
;    TITLE OF INVENTION:  INHIBITORS OF APOPTOSIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/569,749
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brezner, David J.
;      REGISTRATION NUMBER:  24,774
;      REFERENCE/DOCKET NUMBER:  A-62464/DJB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)781-1989
;      TELEFAX:  (415)398-3249
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  604 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-569-749-4

  Query Match             37.4%;  Score 472.5;  DB 4;  Length 604;
  Best Local Similarity   31.0%;  Pred. No. 5.9e-42;
  Matches  111;  Conservative   40;  Mismatches   80;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58

Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106

Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHFEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159

Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN---------------------------------------------- 166

Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ-----------------------------------------------REISPEE 178

Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236

Db        547 QLRRLQEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604


RESULT 14
PCT-US96-12860-4
; Sequence 4, Application PC/TUS9612860
;  GENERAL INFORMATION:
;    APPLICANT:  TULARIK, INC.
;    TITLE OF INVENTION:  INHIBITORS OF APOPTOSIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/12860
;      FILING DATE:  06 AUG 1996
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. Serial Nos. 08/512,946 & 08/569,749
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brezner, David J.
;      REGISTRATION NUMBER:  24,774
;      REFERENCE/DOCKET NUMBER:  A-62464/DJB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)781-1989
;      TELEFAX:  (415)398-3249
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  604 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-12860-4

  Query Match             37.4%;  Score 472.5;  DB 5;  Length 604;
  Best Local Similarity   31.0%;  Pred. No. 5.9e-42;
  Matches  111;  Conservative   40;  Mismatches   80;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58

Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106

Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHFEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159

Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN---------------------------------------------- 166

Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ-----------------------------------------------REISPEE 178
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Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
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Db        547 QLRRLQEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604


RESULT 15
US-08-511-485-6
; Sequence 6, Application US/08511485
; Patent No. 5919912
;  GENERAL INFORMATION:
;    APPLICANT:  Korneluk, Robert G.
;    APPLICANT:  Mackenzie, Alexander E.
;    APPLICANT:  Baird, Stephen
;    TITLE OF INVENTION:  MAMMALIAN IAP GENE FAMILY, PRIMERS,
;    TITLE OF INVENTION:  PROBES, AND DETECTION METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/511,485
;      FILING DATE:  04-AUG-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  07540/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  604 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  both
;    MOLECULE TYPE:  protein
US-08-511-485-6

  Query Match             36.9%;  Score 466.5;  DB 2;  Length 604;
  Best Local Similarity   30.7%;  Pred. No. 2.6e-41;
  Matches  110;  Conservative   40;  Mismatches   81;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||  ||  |  |  || |||| |||| :|  | |:|| | |||  |:  :||| |
Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106
              ||||:| |:||:  || |:|  :     ||   |      :|  :|     |
Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHLEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159
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Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN------------------------------------------- 166
                      | | | |
Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ-----------------------------------------------REISPEE 178
              |||||                                               ::  ||
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Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||| ||: ||:|||: :::|||||||| || || :: :||:| : |    | |:|
Db        547 QLRRLPEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604


Search completed: June 19, 2003, 10:09:51
Job time : 17 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:05 ; Search time 35 Seconds
(without alignments)
898.490 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264
Sequence: 1 MTGYEARLITFGTWMYSVNK.....VDRCPMCSAVIDFKQRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1264	100.0	236	21	AAY81440	Human TIAP (an inh
2	1264	100.0	236	23	AAU75066	Human testes speci
3	1259	99.6	236	22	AAE00365	Human IAP-like pro
4	1259	99.6	464	23	AAU75747	Human Inhibitor of
5	1241	98.2	236	22	AAE00366	Chimpanzee IAP-lik
6	1237	97.9	236	22	AAE00367	Gorilla IAP-like p
7	1052	83.2	278	23	AAO20511	Protein of APP rel
8	1052	83.2	497	18	AAW19581	Human apoptosis in
9	1052	83.2	497	19	AAW69294	Human XIAP protein
10	1052	83.2	497	21	AAY99985	Human X-linked inh
11	1052	83.2	497	23	ABG65663	Human inhibitor of
12	1049	83.0	497	21	AAY59451	Human XIAP protein
13	1028	81.3	496	18	AAW19745	Mouse inhibitor of
14	989	78.2	496	18	AAW19584	Mouse apoptosis in
15	989	78.2	496	19	AAW69297	Murine XIAP protei
16	989	78.2	496	23	ABG65666	Mouse inhibitor of
17	472.5	37.4	604	18	AAW19747	Human inhibitor of
18	472.5	37.4	604	18	AAW13546	Human c-IAP2. Hom
19	472.5	37.4	604	20	AAY52703	Human cellular inh
20	472.5	37.4	604	20	AAY33997	Human cellular inh
21	466.5	36.9	604	18	AAW19582	Human apoptosis in
22	466.5	36.9	604	19	AAW69295	Human HIAP-1 prote
23	466.5	36.9	604	23	ABG65664	Human inhibitor of
24	459	36.3	116	22	AAE00364	Rhesus IAP-like pr
25	458.5	36.3	438	17	AAW04583	Human inhibitor of
26	458.5	36.3	618	18	AAW19746	Human inhibitor of
27	458.5	36.3	618	18	AAW13545	Human c-IAP1. Hom
28	458.5	36.3	618	20	AAY33998	Human cellular inh
29	455.5	36.0	600	19	AAW69298	Murine HIAP-1 prot
30	454.5	36.0	618	18	AAW19583	Human apoptosis in
31	454.5	36.0	618	19	AAW69296	Human HIAP-2 prote
32	454.5	36.0	618	23	ABG65665	Human inhibitor of
33	443	35.0	116	22	AAE00361	Chimpanzee IAP-lik
34	443	35.0	612	18	AAW13555	Murine c-IAP. Mus
35	443	35.0	612	19	AAW69299	Murine HIAP-2 prot
36	440	34.8	116	22	AAE00363	Gorilla IAP-like p
37	440	34.8	116	22	AAE00369	Baboon IAP-like pr
38	438	34.7	116	22	AAE00360	Baboon IAP-like pr
39	437	34.6	591	18	AAW19586	Mouse apoptosis in
40	437	34.6	591	23	ABG65668	Mouse inhibitor of
41	436.5	34.5	115	22	AAE00362	Cynomolgus IAP-lik
42	435	34.4	116	22	AAE00359	Human IAP-like pro
43	433.5	34.3	602	23	ABG65667	Mouse inhibitor of
44	429.5	34.0	602	18	AAW19585	Mouse apoptosis in
45	404	32.0	498	18	AAW19748	Drosophila inhibit

ALIGNMENTS

RESULT 1
AAY81440
ID AAY81440 standard; Protein; 236 AA.
XX
AC AAY81440;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human TIAP (an inhibitor of apoptosis).
XX
KW TIAP; inhibitor of apoptosis protein; IAP; X-linked IAP; XIAP;
KW internal ribosome entry site; IRES; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB01415.
XX
PR 24-JUL-1998; 98US-0121979.
PR 14-JUN-1999; 99US-0332319.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
XX
DR WPI; 2000-338644/29.
DR N-PSDB; AAA06940.
XX

PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer -
XX
PS Disclosure; Page 82; 87pp; English.
XX
CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining
CC the amount of translation from the XIAP IRES reporter cistron exposed to
CC the compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation from the exposed
CC XIAP IRES reporter cistron indicates a compound that increases XIAP
CC IRES-dependent (cap independent) translation. XIAP protein plays a
CC critical role in the regulation of apoptosis by suppressing activation
CC of downstream caspase-3 and caspase-7. Compounds identified by the
CC method which decrease XIAP IRES-dependent translation (thus leading to
CC reduced expression of XIAP and hence increasing apoptosis) can be used
CC for treating cancer. The methods can also be used for the identification
CC of agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease; islet
CC cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP: AAY81440). Such constructs may be used
CC in gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents human TIAP (an inhibitor of apoptosis protein), DNA encoding
CC which may be used in an expression vector comprising a XIAP IRES
CC element.
XX
SQ Sequence 236 AA;

Query Match 100.0%; Score 1264; DB 21; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.1e-119;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
Db 1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy 61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
Db 61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy 121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
Db 121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Qy 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
Db 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236

RESULT 2
AAU75066
ID AAU75066 standard; Protein; 236 AA.
XX
AC AAU75066;
XX
DT 23-APR-2002 (first entry)
XX
DE Human testes specific inhibitor of apoptosis (TIAP) protein.
XX
KW TIAP; apoptosis; testes specific inhibitor of apoptosis;
KW human; apoptotic; cytostatic; anti-infertility; contraceptive;
KW chromosome 12q22-23; transgenic animal; antibody; immunogen;
KW testicular cell; testicular cancer; cancer; male infertility;
KW male birth control; XIAP.
XX
OS Homo sapiens.
XX
PN US6331412-B1.
XX
PD 18-DEC-2001.
XX
PF 29-JAN-1999; 99US-0239867.
XX
PR 29-JAN-1998; 98US-073001P.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Lagace M;
XX
DR WPI; 2002-105275/14.
DR N-PSDB; ABK13197.
XX
PT Nucleic acids encoding a testis specific apoptosis inhibitor protein
PT (TIAP) useful for treating testicular cancers, cancers in
PT non-testicular tissues, male infertility, and for achieving male birth
PT control -
XX
PS Example 4; Fig 4B; 29pp; English.
XX
CC This invention relates to a novel isolated nucleic acid molecule
CC encoding a TIAP polypeptide (testes-specific inhibitor of apoptosis)
CC protein. This gene is a homologue of the X-linked XIAP gene and is
CC located on chromosome 12q22-23. The nucleotide and protein sequences of
CC the invention and vectors containing these sequences may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate TIAP expression. Additionally, the nucleotide sequence may
CC be used to express the TIAP protein by recombinant methods. Conversely,
CC antisense nucleic acid molecules may be administered to down-regulate
CC TIAP expression. The nucleotide sequence, may also be used to design DNA
CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
CC detect and quantitate the presence of similar nucleic acid sequences in
CC samples, to identify patients who may be in need of restorative therapy.
CC Through the production of transgenic animals and cells, the sequences
CC may also be used to study the expression and function of TIAP proteins
CC and their role in metabolism. The TIAP polypeptides may be used to
CC produce antibodies against TIAP and maybe used to identify modulators
CC (agonists and antagonists) of TIAP expression and activity. An anti-TIAP
CC antibody or antagonist may also be used to down-regulate TIAP expression
CC and activity. The reagents may be used in this way for the treatment of
CC excessive or insufficient apoptosis, particularly in testicular cells.
CC In particular they are useful in diagnosing and treating testicular
CC cancers, cancers in non-testicular tissues, male infertility, and for
CC achieving male birth control. The present sequence represents the
CC human TIAP protein sequence of the invention.
XX
SQ Sequence 236 AA;

Query Match 100.0%; Score 1264; DB 23; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.1e-119;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
Db 1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy 61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
Db 61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy 121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
Db 121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Qy 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
Db 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236

```
RESULT 3
AAE00365
ID   AAE00365 standard; Protein; 236 AA.
XX
AC   AAE00365;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Human IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
XX
KW   Human; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KW   chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
KW   TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KW   cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KW   T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KW   retinal degeneration; hyperferritinaemia-cataract syndrome; cancer;
KW   autoimmune disease; diabetes; multiple sclerosis; cytostatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          7..70
FT                   /label= BIR_domain
FT                   /note= "Baculovirus iap repeat"
FT   Domain          188..223
FT                   /label= RING_finger_domain
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PN   WO200123568-A2.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US26735.
XX
PR   30-SEP-1999;   99US-0157169.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Duckett C,  Mir SS;
XX
DR   WPI; 2001-258135/26.
DR   N-PSDB; AAD03581.
XX
PT   Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT   transforming growth factor beta receptor modulating activity, and the
PT   nucleic acids that encode them, useful for treating, e.g. diabetes and
PT   multiple sclerosis -
XX
PS   Claim 1; Fig 2; 108pp; English.
XX
CC   The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
CC   (ILP-2). The hILP-2 gene is located on chromosome 19q13.3-q13.4.
CC   ILP-2 comprises a single amino-terminal domain known as baculovirus iap
CC   repeat (BIR), followed by a spacer region and a carboxy-terminal ring
CC   finger domain. It interacts with transforming growth factor beta
CC   receptor (TGFbetaR) and modulates TGFbetaR activity. It also potently
CC   inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and
CC   Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2
CC   is used in the area of genetic testing for predisposition to diseases,
CC   such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
CC   glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
CC   and hyperferritinaemia-cataract syndrome owing to an ILP-2 deletion or
CC   mutation. The ILP is also used in the treatment of diseases associated
CC   with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
CC   diabetes and multiple sclerosis and neurodegenerative diseases including
CC   retinal degeneration. The ILP-2 gene is also used in gene therapy for
CC   treating patients suffering from ILP-2 gene deletions or mutations.
XX
SQ   Sequence   236 AA;

  Query Match            99.6%;  Score 1259;  DB 22;  Length 236;
  Best Local Similarity  99.6%;  Pred. No. 3.5e-119;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQEEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 4
AAU75747
ID   AAU75747 standard; Protein; 464 AA.
XX
AC   AAU75747;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human Inhibitor of apoptosis protein 7 (IAPL7) protein.
XX
KW   Human; inhibitor of apoptosis 7; IAPL7; cytostatic;
KW   antiapoptotic; IAP; apoptosis; V-Rel; cancer; NF-kappaB;
KW   chromosome 19; vaccine; gene therapy; hyperproliferative disease;
KW   transgenic animal; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..133
FT                   /note= "This sequence is specifically claimed
FT                   in claim 1 of the specification and is encoded
FT                   by the nucleic acid represented in ABK14678"
XX
PN   WO200210381-A1.
XX
PD   07-FEB-2002.
XX
PF   18-JUL-2001; 2001WO-EP08287.
XX
PR   28-JUL-2000; 2000EP-0116452.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Hentsch B;
XX
DR   WPI; 2002-188741/24.
DR   P-PSDB; ABK14677.
XX
PT   New inhibitor of apoptosis proteins and polynucleotides useful in
PT   vaccines for inducing an immune response against hyperproliferative
PT   diseases e.g. cancer  -
XX
PS   Claim 1; Page 35-36; 41pp; English.
XX
CC   This invention relates to the nucleic acid and protein sequences of a
CC   novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences
CC   have homology to the IAP (inhibitors of apoptosis) gene family which
CC   are thought to inhibit proteins by regulating the anti-apoptotic
CC   activity of the V-Rel and NF-kappaB family of transcription factors.
CC   The gene for IAPL7 is located on human chromosome 19. The nucleic acids
CC   of the invention are useful for screening to identify compounds that
CC   stimulate or inhibit the function or level of IAPL7, where the
CC   identified compounds are useful for treating hyper-proliferative
CC   diseases such as cancer. The protein sequences may also be used to
CC   identify membrane bound or soluble receptors of IAPL7 by standard
CC   receptor binding techniques. Nucleic acids encoding IAPL7, may be used
```

CC as hybridisation probes for cDNA and genomic DNA, or as primers for
CC nucleic acid amplification reaction and the primers and probes may also
CC be used to isolate full-length cDNAs and genomic clones encoding IAPL7.
CC The nucleic acid sequences are useful as diagnostic reagents for
CC diagnosing a disease or a susceptibility to a disease by detecting
CC mutations in the associated gene. The nucleic acid sequence is useful
CC for chromosome localisation and tissue expression studies and is also
CC useful for producing transgenic animals. The IAPL7 protein sequence may
CC also be used to generate an anti-IAPL7 antibody which is useful in
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and protein in cells. The sequences of the invention
CC are also useful as vaccines for inducing an immunological response in a
CC mammal. The present sequence represents the human inhibitor of apoptosis
CC 7 (IAP7) protein of the invention.
XX
SQ Sequence 464 AA;

Query Match 99.6%; Score 1259; DB 23; Length 464;
Best Local Similarity 99.6%; Pred. No. 9e-119;
Matches 235; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 288

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 348

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 408

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        409 RRLQEEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 464
```

RESULT 5
AAE00366
ID AAE00366 standard; Protein; 236 AA.
XX
AC AAE00366;
XX
DT 19-JUN-2001 (first entry)
XX
DE Chimpanzee IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
XX
KW Chimpanzee; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KW transforming growth factor beta receptor; TGFbetaR;
KW c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KW retinal degeneration; hyperferritinaemia-cataract syndrome; cancer;
KW autoimmune disease; diabetes; multiple sclerosis; cytostatic.
XX
OS Pan troglodytes.
XX
PN WO200123568-A2.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US26735.
XX
PR 30-SEP-1999; 99US-0157169.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Duckett C, Mir SS;
XX
DR WPI; 2001-258135/26.
DR N-PSDB; AAD03582.
XX
PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
PT multiple sclerosis -
XX
PS Claim 1; Fig 2; 108pp; English.
XX
CC The present sequence is chimpanzee inhibitor of apoptosis (IAP)-like
CC protein-2 (ILP-2). ILP-2 comprises a single amino-terminal domain
CC known as baculovirus iap repeat (BIR), followed by a spacer region and a
CC carboxy-terminal ring finger domain. It interacts with transforming
CC growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity.
CC It also potently inhibits apoptosis induced by overexpression of Bax or
CC by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)
CC activity. ILP-2 is used in the area of genetic testing for predisposition
CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
CC and hyperferritinaemia-cataract syndrome owing to an ILP-2 deletion or
CC mutation. The ILP is also used in the treatment of diseases associated
CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
CC diabetes and multiple sclerosis and neurodegenerative diseases including
CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
CC treating patients suffering from ILP-2 gene deletions or mutations.
XX
SQ Sequence 236 AA;

Query Match 98.2%; Score 1241; DB 22; Length 236;
Best Local Similarity 97.9%; Pred. No. 2.3e-117;
Matches 231; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYFVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRINDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENESNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||:||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQDEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
```

RESULT 6
AAE00367
ID AAE00367 standard; Protein; 236 AA.
XX
AC AAE00367;
XX
DT 19-JUN-2001 (first entry)
XX
DE Gorilla IAP-like protein-2 (ILP-2) with TGFbetaR modulating activity.
XX
KW Gorilla; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KW transforming growth factor beta receptor; TGFbetaR; cytostatic;
KW c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KW retinal degeneration; hyperferritinaemia-cataract syndrome; cancer;
KW autoimmune disease; diabetes; multiple sclerosis.
XX
OS Gorilla gorilla.
XX
PN WO200123568-A2.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US26735.
XX

PR 30-SEP-1999; 99US-0157169.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Duckett C, Mir SS;
XX
DR WPI; 2001-258135/26.
DR N-PSDB; AAD03583.
XX
PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
PT multiple sclerosis -
XX
PS Claim 1; Fig 2; 108pp; English.
XX
CC The present sequence is gorilla inhibitor of apoptosis (IAP)-like
CC protein-2 (ILP-2) cDNA. ILP-2 comprises a single amino-terminal domain
CC known as baculovirus iap repeat (BIR), followed by a spacer region and a
CC carboxy-terminal ring finger domain. It interacts with transforming
CC growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity.
CC It also potently inhibits apoptosis induced by overexpression of Bax or
CC by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)
CC activity. ILP-2 is used in the area of genetic testing for predisposition
CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
CC and hyperferritinaemia-cataract syndrome owing to an ILP-2 deletion or
CC mutation. The ILP is also used in the treatment of diseases associated
CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
CC diabetes and multiple sclerosis and neurodegenerative diseases including
CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
CC treating patients suffering from ILP-2 gene deletions or mutations.
XX
SQ Sequence 236 AA;

Query Match 97.9%; Score 1237; DB 22; Length 236;
Best Local Similarity 97.0%; Pred. No. 5.9e-117;
Matches 229; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |||||| |||||||||||||||||||||||||:|||||||||||||||||||||||
Db          1 MTGYEAWLITFGTWMYSVNKEQLARAGFYAIGQEDKIQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||||||:||||||:||||||||||||||||||||||||||| ||||||||||||||
Db        121 MGFDFKDIKKIMEEKIQTSGSNYKTLEVLVADLVSAQKDTTENESNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||:||||||||||||||||||||||||:||||||||||
Db        181 RRLQEEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCNAVIDFKQRVFMS 236
```

RESULT 7
AAO20511
ID AAO20511 standard; Protein; 278 AA.
XX
AC AAO20511;
XX
DT 27-JUN-2002 (first entry)
XX
DE Protein of APP related human homologue hCP35211.
XX
KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP11345.
XX
PR 29-SEP-2000; 2000US-236893P.
PR 14-JUN-2001; 2001US-298309P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWHM, Zusman S;
XX
DR WPI; 2002-315796/35.
DR N-PSDB; AAK99405.
XX
PT New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease -
XX
PS Example 4; Page 112; 129pp; English.
XX
CC The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This sequence represents the
CC protein of the APP related human homologue hCP35211.
XX
SQ Sequence 278 AA;

Query Match 83.2%; Score 1052; DB 23; Length 278;
Best Local Similarity 80.1%; Pred. No. 4.1e-98;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||:|: |||:||||||||.:||| ||||||||
Db         43 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 102

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        103 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 162

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:||||||||:|||| ::| :|||||:||| || |
Db        163 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 222

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||::|||
Db        223 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 278
```

RESULT 8
AAW19581
ID AAW19581 standard; Protein; 497 AA.
XX
AC AAW19581;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor XIAP.
XX
KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;

KW ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
KW diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 26..93
FT /label= BIR-1
FT Domain 163..230
FT /label= BIR-2
FT Domain 265..330
FT /label= BIR-3
FT Domain 439..484
FT /label= Ring_zinc_finger
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB01022.
XX
PR 22-DEC-1995; 95US-0576956.
PR 04-AUG-1995; 95US-0511485.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
DR WPI; 1997-154262/14.
DR N-PSDB; AAT70836.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
PS Claim 27; Page 68-70; 219pp; English.
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The XIAP amino acid sequence was deduced from the xiap gene
CC (AAT70836) isolated from a human foetal brain cDNA library.
CC IAP polypeptides can be expressed in host cells (in vitro or in
CC vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or
CC as having AIDS, a neurodegenerative disease, a myelodysplastic
CC syndrome or an ischaemic injury, seleted from myocardial infarction,
CC stroke, reperfusion injury, or a toxin-induced liver disease.
XX
SQ Sequence 497 AA;

Query Match 83.2%; Score 1052; DB 18; Length 497;
Best Local Similarity 80.1%; Pred. No. 9.3e-98;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: ||||||:||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:||||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:|||||||||:|||| ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497
```

RESULT 9
AAW69294
ID AAW69294 standard; Protein; 497 AA.
XX
AC AAW69294;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human XIAP protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein.
XX
OS Homo sapiens.
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI; 1998-467164/40.
DR N-PSDB; AAV55038.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
PS Disclosure; Fig 1; 147pp; English.
XX
CC This sequence is the human XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharnyx, thyroid,central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 497 AA;

Query Match 83.2%; Score 1052; DB 19; Length 497;
Best Local Similarity 80.1%; Pred. No. 9.3e-98;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: ||||||:||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:||||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:|||||||||:|||| ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441
```

```
Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||||||||||||| ||:||:||||||||||||||||:||||  || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497
```

RESULT 10
AAY99985
ID AAY99985 standard; Protein; 497 AA.
XX
AC AAY99985;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human X-linked inhibitor of apoptosis.
XX
KW X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880;
KW antisense; antiinflammatory; cytostatic; tumour.
XX
OS Homo sapiens.
XX
PN US6087173-A.
XX
PD 11-JUL-2000.
XX
PF 09-SEP-1999; 99US-0392580.
XX
PR 09-SEP-1999; 99US-0392580.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM, Ackermann EJ;
XX
DR WPI; 2000-498201/44.
DR N-PSDB; AAA64901.
XX
PT Antisense compound useful for research reagents, diagnostics,
PT prophylaxis and for treating disorders associated with X-linked
PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
PT apoptosis -
XX
PS Example 13; Column 43-48; 33pp; English.
XX
CC The present invention relates to antisense oligonucleotides designed to
CC inhibit expression of the human X-linked inhibitor of apoptosis
CC (the present sequence). Modified phosphorothioate 2'-MOE
CC oligonucleotides are more effective inhibitors than unmodified
CC oligonucleotides. The oligonucleotides may be used to inhibit X-linked
CC inhibitor of apoptosis expression in cells and tissues in vitro. The
CC oligonucleotides are also useful for treating animals or humans, prone
CC to a disease associated with X-linked inhibitor of apoptosis. The
CC oligonucleotides may also be used prophylactically to prevent
CC infection, inflammation or tumour formation.
XX
SQ Sequence 497 AA;

Query Match 83.2%; Score 1052; DB 21; Length 497;
Best Local Similarity 80.1%; Pred. No. 9.3e-98;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| ||||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|||||||:|| ||||||:|||||||||:|||| ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||||||||||||| ||:||:||||||||||||||||:||||  || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497
```

RESULT 11
ABG65663
ID ABG65663 standard; Protein; 497 AA.
XX
AC ABG65663;
XX
DT 26-AUG-2002 (first entry)
XX
DE Human inhibitor of apoptosis, XIAP.
XX
KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
OS Homo sapiens.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA01379.
XX
PR 28-SEP-2000; 2000US-0672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
DR WPI; 2002-479562/51.
DR N-PSDB; ABK93869.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases -
XX
PS Example 12; Fig 1; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence.
XX
SQ Sequence 497 AA;

Query Match 83.2%; Score 1052; DB 23; Length 497;
Best Local Similarity 80.1%; Pred. No. 9.3e-98;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321
```

```
Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|||||:|| ||||||:|||||||||:|||| ::| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:||||||||||||||:|||| || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 12
AAY59451
ID   AAY59451 standard; Protein; 497 AA.
XX
AC   AAY59451;
XX
DT   24-MAR-2000  (first entry)
XX
DE   Human XIAP protein sequence.
XX
KW   Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW   transforming growth factor-beta activated kinase 1; monocyte migration;
KW   TAK1 binding protein 1; extracellular matrix protein production;
KW   cell growth inhibitor; beta-amyloid protein deposition;
KW   immunosuppression; Transforming growth factor-beta.
XX
OS   Homo sapiens.
XX
PN   JP11326328-A.
XX
PD   26-NOV-1999.
XX
PF   13-MAY-1998;   98JP-0130378.
XX
PR   13-MAY-1998;   98JP-0130378.
XX
PA   (MATS/) MATSUMOTO K.
XX
DR   WPI; 2000-078337/07.
DR   N-PSDB; AAZ48862.
XX
PT   Screening a substance which inhibits combination of the X-linked
PT   inhibitor of apoptosis protein  -
XX
PS   Claim 3; Page 28-30; 43pp; Japanese.
XX
CC   This sequence represents the human XIAP protein.
CC   The invention relates to a method for screening a substance inhibiting
CC   the formation of a complex between XIAP and TAB1, in which X-linked
CC   inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
CC   activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
CC   tested are contacted with each other and then the presence or formation
CC   of a complex between XIAP and TAB1 is detected. The substance can be used
CC   as a drug for extracellular matrix protein production enhancement, cell
CC   growth inhibition, monocyte migration, physiologically active substance
CC   induction, immunosuppression, and beta-amyloid protein deposition. A
CC   substance inhibiting the formation of a complex between TAB1 and XIAP as
CC   well as between XIAP and TGF-beta (Transforming growth factor-beta) type
CC   I and/or type II receptor is useful as a drug.
XX
SQ   Sequence   497 AA;

  Query Match             83.0%;  Score 1049;  DB 21;  Length 497;
  Best Local Similarity   80.1%;  Pred. No. 1.9e-97;
  Matches  189;  Conservative   24;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321
```

```
Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|||||:|| ||||||:|||||||||:|||| :| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMPDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:||||||||||||||:|||| || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497


RESULT 13
AAW19745
ID   AAW19745 standard; Protein; 496 AA.
XX
AC   AAW19745;
XX
DT   16-SEP-1997  (first entry)
XX
DE   Mouse inhibitor of apoptosis protein homologue MIHA.
XX
KW   Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
KW   degenerative disease; infectious disease; autoimmune disease;
KW   cancer; therapy; diagnosis.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          26..93
FT                   /label= BIR
FT   Region          163..230
FT                   /label= BIR
FT   Region          264..330
FT                   /label= BIR
FT   Region          448..485
FT                   /label= RING_finger
XX
PN   WO9723501-A1.
XX
PD   03-JUL-1997.
XX
PF   20-DEC-1996;   96WO-AU00827.
XX
PR   22-DEC-1995;   95AU-0007275.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Vaux DL;
XX
DR   WPI; 1997-350966/32.
DR   N-PSDB; AAT72710.
XX
PT   Isolated protein homologues of viral inhibitors of apoptosis - used
PT   to modulate apoptosis for treatment of degenerative, infectious or
PT   autoimmune diseases and cancer
XX
PS   Claim 7; Page 44-47; 136pp; English.
XX
CC   Mammalian IAP homologue A (MIHA) (AAW19745) is a murine homologue of
CC   baculovirus inhibitor of apoptosis protein (IAP).  Its amino acid
CC   sequence was deduced from a cDNA clone (see also AAT72710) isolated
CC   from a mouse liver cDNA library on the basis of homology to Orgyia
CC   pseudotsuguta polyhedrosis virus IAP BIR and RING finger amino acid
CC   motifs (see also AAW19744).  IAP homologues (see also AAW19746-52) and
CC   their derivatives and chemical analogues can be used in methods for
CC   modulating apoptosis in animal cells, specifically for treatment,
CC   by inhibition, of degenerative and infectious disease or, by
CC   promotion, of cancer and autoimmune disease.
XX
SQ   Sequence   496 AA;
```

```
  Query Match             81.3%;  Score 1028;  DB 18;  Length 496;
  Best Local Similarity   78.4%;  Pred. No. 2.5e-95;
  Matches  185;  Conservative   26;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||  |||||||||||||||:|: |||:||||||||| :||| ||||||||
Db        261 MAEYEARIVTFGTWTSSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              |||||||||:||| |||||||| ||| :| :| :||||||:| |||| |||:|||||
Db        321 KWYPGCKYLLDEKGQEYINNIHLTHSLEESLGRTAEKTPSLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:||||||:| :||||:||||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDIKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||||:|||| || |||::|||
Db        441 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 496


RESULT 14
AAW19584
ID   AAW19584 standard; Protein; 496 AA.
XX
AC   AAW19584;
XX
DT   02-SEP-1997  (first entry)
XX
DE   Mouse apoptosis inhibitor M-XIAP.
XX
KW   Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
KW   M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
KW   ischaemia; myocardial infarction; stroke;
KW   reperfusion injury; toxin-induced liver disease; gene therapy;
KW   diagnosis.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          26..93
FT                   /label= BIR-1
FT   Domain          163..230
FT                   /label= BIR-2
FT   Domain          264..329
FT                   /label= BIR-3
FT   Domain          438..483
FT                   /label= Ring_zinc_finger
XX
PN   WO9706255-A2.
XX
PD   20-FEB-1997.
XX
PF   05-AUG-1996;   96WO-IB01022.
XX
PR   22-DEC-1995;   95US-0576956.
PR   04-AUG-1995;   95US-0511485.
XX
PA   (UYOT-) UNIV OTTAWA.
XX
PI   Baird S,  Korneluk RG,  Liston P,  Mackenzie AE;
XX
DR   WPI; 1997-154262/14.
DR   N-PSDB; AAT70839.
XX
PT   Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT   to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT   of susceptibility to apoptotic disease
XX
PS   Claim 27; Page 79-80; 219pp; English.
XX
CC   Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC   M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC   are inhibitors of apoptosis (IAP) and which are characterised by
CC   the presence of a ring zinc finger domain (see also AAW19587) and at
CC   least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC   The M-XIAP amino acid sequence was deduced from the m-xiap gene
CC   (AAT70839) isolated from a mouse embryo cDNA library.  The IAP
CC   olypeptides can be expressed in host cells (in vitro or in
CC   vivo) and used in methods for treating diseases and disorders
CC   involving apoptosis, esp. in a human diagnosed as HIV-positive or
CC   as having AIDS, a neurodegenerative disease, a myelodysplastic
CC   syndrome or an ischaemic injury, seleted from myocardial infarction,
CC   stroke, reperfusion injury, or a toxin-induced liver disease.
XX
SQ   Sequence   496 AA;

  Query Match             78.2%;  Score 989;  DB 18;  Length 496;
  Best Local Similarity   75.8%;  Pred. No. 2.2e-91;
  Matches  179;  Conservative   27;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||:||||||||||||||||:|: |||:||||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              | ||||||||:||| ||||||||  || :| :| :||| |||:| |||| |||:|||||
Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:||||||:| :||||:||||||||| ||:| :|||||::|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| |||||||||||:|||| || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496


RESULT 15
AAW69297
ID   AAW69297 standard; Protein; 496 AA.
XX
AC   AAW69297;
XX
DT   13-NOV-1998  (first entry)
XX
DE   Murine XIAP protein.
XX
KW   Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW   proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
XX
OS   Mus sp.
XX
PN   WO9835693-A2.
XX
PD   20-AUG-1998.
XX
PF   13-FEB-1998;   98WO-IB00781.
XX
PR   13-FEB-1997;   97US-0800929.
XX
PA   (UYOT-) UNIV OTTAWA.
XX
PI   Baird S,  Korneluk R,  Liston P,  Mackenzie AE,  Pratt C;
PI   Tsang B;
XX
DR   WPI; 1998-467164/40.
DR   N-PSDB; AAV55041.
XX
PT   Inducing apoptosis in proliferative mammalian cells with inhibitor
PT   of IAP or NAIP polypeptide - also methods for prognosis based on
PT   presence of IAP and NAIP, specifically applied to cancers involving
PT   p53 mutations
XX
PS   Disclosure; Fig 4; 147pp; English.
```

XX
CC This sequence is the murine XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharnyx, thyroid,central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 496 AA;

Query Match 78.2%; Score 989; DB 19; Length 496;
Best Local Similarity 75.8%; Pred. No. 2.2e-91;
Matches 179; Conservative 27; Mismatches 30; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||:|||
Db        261 MAEYEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              | ||||||||:||| |||||||||  || :| :| :||| |||:| |||| |||:|||||
Db        321 KCYPGCKYLLDEKGQEYINNIHLTHPLEESLGRTAEKTPPLTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:|| |||:||||||:| :||||:|||||||||| ||:| :||||||:|| || |
Db        381 MGFSFKDLKKTMEEKIQTSGSSYLSLEVLIADLVSAQKDNTEDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||| |||||| ||:|| ||||| ||||||||||:|||| || | |::|||
Db        441 RRLQEEKLSKICMDRNIAIVFFPCGHLATCKQCAEAVDKCPMCYTVITFNQKIFMS 496
```

Search completed: June 19, 2003, 10:10:34
Job time : 37 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:04 ; Search time 18 Seconds
(without alignments)
1260.429 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264
Sequence: 1 MTGYEARLITFGTWMYSVNK.....VDRCPMCSAVIDFKQRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1049	83.0	497	2	S69544	apoptosis inhibito
2	466.5	36.9	604	2	S68449	apoptosis inhibito
3	454.5	36.0	618	2	S68450	apoptosis inhibito
4	427	33.8	358	2	JC5964	apoptosis inhibito
5	402.5	31.8	497	2	S69545	apoptosis inhibito
6	400	31.6	496	2	S68452	apoptosis inhibito
7	373.5	29.5	298	2	JC7568	kidney inhibitor o
8	314.5	24.9	275	2	A45679	inhibitor-of-apopt
9	312.5	24.7	268	2	T10304	inhibitor of apopt
10	312.5	24.7	268	2	A53989	apoptosis-inhibiti
11	222.5	17.6	1447	2	T42628	neuronal apoptosis
12	209.5	16.6	1232	2	A55478	neuronal apoptosis
13	205	16.2	208	2	T03183	probable apoptosis
14	200.5	15.9	155	2	T30489	apoptosis inhibito
15	193.5	15.3	150	2	T28409	ORF MSV248 probabl
16	192	15.2	292	2	T41772	IAP1 orf27 - Bomby
17	182	14.4	275	2	T10310	apoptosis-inhibiti
18	179	14.2	286	2	D36828	orf13 protein - Au
19	165.5	13.1	249	2	H72858	apoptosis inhibito
20	161.5	12.8	249	2	T41814	IAP2 orf71 - Bomby
21	147.5	11.7	316	2	T32659	hypothetical prote
22	144	11.4	383	2	F96582	hypothetical prote
23	143	11.3	263	2	T22135	hypothetical prote
24	139	11.0	711	2	C84767	hypothetical prote
25	133	10.5	329	2	T28403	ORF MSV242 probabl
26	128	10.1	4845	2	T31067	BIR repeat contain
27	127.5	10.1	864	2	T01393	apoptosis inhibito
28	126	10.0	145	2	S77736	probable zinc fing
29	125	9.9	115	2	B96664	probable RING zinc
30	124.5	9.8	347	2	T01044	hypothetical prote
31	122	9.7	785	2	T00474	hypothetical prote
32	120.5	9.5	823	2	D86165	protein F15K9.3 [i
33	119.5	9.5	943	2	S68824	rngB protein, cyto
34	119	9.4	936	2	E71405	probable ankyrin -
35	117	9.3	673	2	T21007	hypothetical prote
36	114.5	9.1	285	2	T05777	hypothetical prote
37	112.5	8.9	234	2	T30427	probable apoptosis
38	111	8.8	433	2	JC7678	RING finger protei
39	110.5	8.7	780	2	T31548	hypothetical prote
40	110	8.7	204	2	T01447	hypothetical prote
41	110	8.7	582	2	S57722	sli-1 protein - Ca
42	110	8.7	585	2	T29654	hypothetical prote
43	109.5	8.7	428	2	T48167	hypothetical prote
44	109.5	8.7	489	2	S71955	MDM2-like p53-bind
45	108.5	8.6	614	2	S42526	finger protein unk

ALIGNMENTS

RESULT 1
S69544
apoptosis inhibitor IAP homolog - human
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C;Accession: S69544; S68451
R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan,
EMBO J. 15, 2685-2694, 1996
A;Title: A conserved family of cellular genes related to the baculovirus iap gene and
A;Reference number: S69544; MUID:96256286; PMID:8654366
A;Accession: S69544
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-497 <DUC>
A;Cross-references: EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g1016688
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: S68451
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-161,'C',163-422,'Q',424-497 <LIS>
A;Cross-references: EMBL:U45880; NID:g1184319; PIDN:AAC50373.1; PID:g1184320
C;Genetics:
A;Gene: ilp
C;Function:
A;Description: apoptotic suppressor
C;Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C;Keywords: apoptosis; zinc finger
F;446-490/Domain: RING finger homology <RRN>

Query Match 83.0%; Score 1049; DB 2; Length 497;
Best Local Similarity 80.1%; Pred. No. 1e-75;
Matches 189; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  ||||: |||||:||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        262 MADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 321

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:|| |||||||| |||  ||:||:||||||:|| |||| |||:|||||
Db        322 KWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTEKTPSLTRRIDDTIFQNPMVQEAIR 381

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||| |||:||||||:|| ||||||:|||||||||:||||:  :| :|||||:||| || |
Db        382 MGFSFKDIKKIMEEKIQISGSNYKSLEVLVADLVNAQKDSMPDESSQTSLQKEISTEEQL 441

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||| ||:||:|||||||||||||||:||||  || |||::|||
Db        442 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS 497
```

RESULT 2
S68449
apoptosis inhibitor hiap-1 - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C;Accession: S68449
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: S68449
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-604 <LIS>
A;Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316
C;Function:
A;Description: apoptotic suppressor
C;Superfamily: RING finger homology
C;Keywords: apoptosis; zinc finger
F;553-597/Domain: RING finger homology <RNG>

Query Match 36.9%; Score 466.5; DB 2; Length 604;
Best Local Similarity 30.7%; Pred. No. 2.5e-29;
Matches 110; Conservative 40; Mismatches 81; Indels 127; Gaps 8;

```
Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||  ||  |  |  || |||| |||| :|  | |:|| | |||  |:  :||| |
Db        252 MQTHAARFKTFFNWPSSVLVNPEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQ 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTPSLTKRIS------- 106
              ||||:| |:||:  || |:|  :     ||  |     :|  :|     |
Db        312 HAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQL-----LSTSDSPGDENAESSIIHLEP 366

Qy        107 ------DTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKD 159
                  | |  | |::  |: |||    ||: :: :|  :| ||: :  || ||::|: :
Db        367 GEDHSEDAIMMNTPVINAAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLDLLNAEDE 426

Qy        160 ---------TTENELN---------------------------------------------- 166
                      | | | |
Db        427 IREEERERATEEKESNDLLLIRKNRMALFQHLTCVIPILDSLLTAGIINEQEHDVIKQKT 486

Qy        167 QTSLQ-----------------------------------------------REISPEE 178
              |||||                                              ::  ||
Db        487 QTSLQARELIDTILVKGNIAATVFRNSLQEAEAVLYEHLFVQQDIKYIPTEDVSDLPVEE 546

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||| ||: ||:|||: :::||||||||| || || :: :||:| : |    | |:|
Db        547 QLRRLPEERTCKVCMDKEVSIVFIPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS 604
```

RESULT 3
S68450
apoptosis inhibitor hiap-2 - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C;Accession: S68450
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: S68450
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-618 <LIS>
A;Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318
C;Function:
A;Description: apoptotic suppressor
C;Superfamily: RING finger homology
C;Keywords: apoptosis; zinc finger
F;567-611/Domain: RING finger homology <RNG>

Query Match 36.0%; Score 454.5; DB 2; Length 618;
Best Local Similarity 29.5%; Pred. No. 2.4e-28;
Matches 104; Conservative 49; Mismatches 83; Indels 117; Gaps 6;

```
Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  | |||| |||| :|: | |:|| | |||  |:  :||| :
Db        266 MQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVE 325

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKT---------PSLTKR 104
              ||||:| |::|:  || |:::  |     ||   |       | ::         |  :
Db        326 HAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSS 385

Qy        105 ISDTIFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE 164
                  :   |::: |: |||:   ||: :  :| |:| ||||:  :|: |::|: :  | |
Db        386 EDAVMMNTPVVKSALEMGFNRDLVKQTVLSKILTTGENYKTVNDIVSALLNAEDEKREEE 445

Qy        165 ----------------------------------------------------LNQTSLQ 171
                                                                   |  ||
Db        446 KEKQAEEMASDDLSLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQ 505

Qy        172 -RE-----------------------------------------------ISPEEPLRRL 183
               ||                                              :| || ||||
Db        506 ARELIDTIWVKGNAAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRL 565

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||: ||:||||: ::|||||||||| |::|| :: :||:|  :|    | |:|
Db        566 QEERTCKVCMDKEVSVVFIPCGHLVVCQECAPSLRKCPICRGIIKGTVRTFLS 618
```

RESULT 4
JC5964
apoptosis inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C;Accession: JC5964
R;Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A;Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (iap)
A;Reference number: JC5964; MUID:98162622; PMID:9501011
A;Accession: JC5964
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STE>
A;Cross-references: GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g2957175
C;Superfamily: RING finger homology
F;307-351/Domain: RING finger homology <RRN>

Query Match 33.8%; Score 427; DB 2; Length 358;
Best Local Similarity 34.3%; Pred. No. 1.9e-26;
Matches 96; Conservative 45; Mismatches 87; Indels 52; Gaps 8;

```
Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  | ||  ||  |  |  |: |||| |||| :|  | |:|| | |||  |:  :||| :
Db         87 MQTYAARFKTFCNWPSSIPVHPEQLASAGFYYMGHSDDVKCFCCDGGLRCWESGDDPWVE 146

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTP----------SLT 102
              ||||:| |.:||:  || |:|: :     ||   |      :|   |           ||
Db        147 HAKWFPRCEYLIRIKGQEFISRVQASYPHLLEQL-----LSTSDNPEDENAEPPNDLSLI 201

Qy        103 KRISDTIFPN-----PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQ 157
              ::    :| :     |:|   :       :    ::::: |||    : ::::   ||
Db        202 RKNRMALFQHLTCVLPILDSLLIARVISEQEHDVIKQKTQTSLQARELIDII---LVKGN 258

Qy        158 KDTT--ENELNQ------------------TSLQREISPEEPLRRLQEEKLCKICMDRY 196
                 |  :| | :                    |    ::| || ||||||: ||:|||:
Db        259 YAATIFKNSLQEIDPMLYKHLFVQQDIKYIPTENVSDLSMEEQLRRLQEERTCKVCMDKE 318

Qy        197 IAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              :::|||||||||| || || :: :||:|   |    | |:|
Db        319 VSIVFIPCGHLVVCKDCAPSLRKCPICRGTIKGTVRTFLS 358
```

RESULT 5
S69545

```
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69545
R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C
EMBO J. 15, 2685-2694, 1996
A;Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A;Reference number: S69544; MUID:96256286; PMID:8654366
A;Accession: S69545
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-497 <DUC>
A;Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117
C;Genetics:
A;Gene: ilp
C;Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F;446-490/Domain: RING finger homology <RRN>

  Query Match            31.8%;  Score 402.5;  DB 2;  Length 497;
  Best Local Similarity  30.9%;  Pred. No. 2.5e-24;
  Matches   89;  Conservative   46;  Mismatches   94;  Indels   59;  Gaps    4;

Qy          5 EARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKW 62
              :||| ||  |  |       ||:|| |     |:|:|||| || :|: :::|| :|||| 
Db        213 DARLRTFTDWPISNIQPASALAQAGLYYQKIGDQVRCFHCNIGLRSWQKEDEPWFEHAKW 272

Qy         63 YPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMG 122
               | |:::|  ||  |:: :  | :   :    |   |:|    :| :      :||: :| 
Db        273 SPKCQFVLLAKGPSYVSEVLATTAANASSPPATAPAPTLQ---ADVLMDEAPAKEALALG 329

Qy        123 FDFKDVKKIMEERIQTSGSNYKTLEVL-------------------------------- 149
               |   |:  :: :: :||  : ||: |
Db        330 IDGGVVRNAIQRKLLSSGCAFSTLDELLHDIFDDAGAGADWRCASREPSAPFIEPCQATT 389

Qy        150 ---------VADLVSAQKDTTENELNQTSLQREI-----------SPEEPLRRLQEEKL 188
                      ||| : |:    |   | : :  ||            | ||  |:|:: :| 
Db        390 SKAASVPIPVADSIPAKPQAAEAVANISKITDEIQKMSVATPNGNLSLEEENRQLKDARL 449

Qy        189 CKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||:|:|  : |||:||||| || ||| :|  |||| | |    | |:|
Db        450 CKVCLDEEVGVVFLPCGHLATCNQCAPSVANCPMCRADIKGFVRTFLS 497


RESULT 6
S68452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C;Accession: S68452; S78528
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: S68452
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-496 <LIS>
A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
R;Baird, S.D.
submitted to the EMBL Data Library, January 1996
A;Reference number: S78528
A;Accession: S78528
A;Molecule type: mRNA
A;Residues: 1-36,'AT',37,'K',39,'L',41-44,'H',46-58,'Q',60-412,'A',414-427,'A',429-496 <
A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
C;Genetics:
A;Cross-references: FlyBase:FBgn0015247
C;Function:
A;Description: apoptotic suppressor
C;Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C;Keywords: apoptosis; zinc finger
F;445-489/Domain: RING finger homology <RNG>

  Query Match            31.6%;  Score 400;  DB 2;  Length 496;
  Best Local Similarity  30.8%;  Pred. No. 3.9e-24;
  Matches   89;  Conservative   46;  Mismatches   94;  Indels   60;  Gaps    4;

Qy          5 EARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKW 62
              :||| ||  |  |       ||:|| |     |:|:|||| || :|: :::|| :|||| 
Db        211 DARLRTFTDWPISNIQPASALAQAGLYYQKIGDQVRCFHCNIGLRSWQKEDEPWFEHAKW 270

Qy         63 YPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMG 122
               | |:::|  ||  |:: :  | :   :    |   |:|    :| :      :||: :| 
Db        271 SPKCQFVLLAKGPAYVSEVLATTAANASSQPATAPAPTLQ---ADVLMDEAPAKEALTLG 327

Qy        123 FDFKDVKKIMEERIQTSGSNYKTLEVL-------------------------------- 149
               |   |:  :: :: :||  : ||: |
Db        328 IDGGVVRNAIQRKLLSSGCAFSTLDELLHDIFDDAGAGAALEVREPPEPSAPFIEPCQAT 387

Qy        150 ----------VADLVSAQKDTTENELNQTSLQREI-----------SPEEPLRRLQEEK 187
                       ||| : |:    |   | : :  ||            | ||  |:|:: : 
Db        388 TSKAASVPIPVADSIPAKPQAAEAVSNISKITDEIQKMSVSTPNGNLSLEEENRQLKDAR 447

Qy        188 LCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||:|:|  : |||:||||| || ||| :|  |||| | |    | |:|
Db        448 LCKVCLDEEVGVVFLPCGHLATCNQCAPSVANCPMCRADIKGFVRTFLS 496


RESULT 7
JC7568
kidney inhibitor of apoptosis protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7568
R;Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A;Title: KIAP, a novel member of the inhibitor of apoptosis protein family.
A;Reference number: JC7568; MUID: 21092523; PMID:11162435
A;Contents: Fetal kidney
A;Accession: JC7568
A;Molecule type: mRNA
A;Residues: 1-298 <LIN>
C;Comment: This protein, a new member of the inhibitor of apoptosis protein family, p
.
C;Genetics:
A;Gene: kiap
A;Map position: 20q13.3
C;Keywords: apoptosis

  Query Match            29.5%;  Score 373.5;  DB 2;  Length 298;
  Best Local Similarity  32.2%;  Pred. No. 2.7e-22;
  Matches   82;  Conservative   42;  Mismatches   72;  Indels   59;  Gaps    9;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |   | || :|  |  :  |  | || |||:  | :|||:|| | ||| :||  :||| : 
Db         84 MGSEELRLASFYDWPLTAEVPPELLAAAGFFHTGHQDKVRCFFCYGGLQSWKRGDDPWTE 143

Qy         59 HAKWYPGCKYLLEEKGHEYINNIHLTRS-LEGALVQTTKKTPSLTKRISDTI-------F 110
              ||||:| |::||  || ::::::  | | | |:      : |     :: ::  
Db        144 HAKWFPSCQFLLRSKGRDFVHSVQETHSQLLGS--WDPWEEPEDAAPVAPSVPASGYPEL 201

Qy        111 PNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSL 170
              | |                :::  |  |  |                      ::    
Db        202 PTPR--------------REVQSESAQEPGG----------------------VSPAEA 224

Qy        171 QRE---ISP------EEPLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCP 221
              ||    : |      |  |||||||: ||:|:|| :::||:|||||| | :||  :  || 
Db        225 QRAWWVLEPPGARDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLV-CAECAPGLQLCP 283

Qy        222 MCSAVIDFKQRVFMS 236
              :| | :  : | |:|
Db        284 ICRAPVRSRVRTFLS 298


RESULT 8
A45679
```

inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C;Species: Cydia pomonella granulosis virus CpGV
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C;Accession: A45679
R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A;Reference number: A45679; MUID:93188168; PMID:8445726
A;Accession: A45679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <CRO>
A;Cross-references: GB:L05494; NID:g289583; PIDN:AAA43835.1; PID:g289584
A;Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 24.9%; Score 314.5; DB 2; Length 275;
Best Local Similarity 27.9%; Pred. No. 1.2e-17;
Matches 65; Conservative 38; Mismatches 61; Indels 69; Gaps 5;

```
Qy          6 ARLITFGTWMYSVNK--EQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKWY 63
              ||: :|  |   : :  ||:| |||:  |  |  :||:| ||| :|:|:: ||||| :|:
Db        110 ARVKSFHNWPRCMKQRPEQMADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHVRWF 169

Qy         64 PGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMGF 123
                | |:   || :|
Db        170 DRCAYVQLVKGRDY---------------------------------------------- 183

Qy        124 DFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPLRRL 183
                |:|:: |     | |             ||     :|  : :| :::|        ::
Db        184 ----VQKVITEACVLPGEN---------TTVSTAAPVSE-PIPETKIEKE-------PQV 222

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              :: ||||||      | |:||||:| | :|| :||:|||  ::    :|: |
Db        223 EDSKLCKICYVEECIVCFVPCGHVVACAKCALSVDKCPMCRKIVTSVLKVYFS 275
```

RESULT 9
T10304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C;Accession: T10304
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-268 <AHR>
A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Query Match 24.7%; Score 312.5; DB 2; Length 268;
Best Local Similarity 27.7%; Pred. No. 1.7e-17;
Matches 64; Conservative 31; Mismatches 57; Indels 79; Gaps 4;

```
Qy          6 ARLITFGTWMYSVNK--EQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKWY 63
              ||| ||  |   : :  |:|| |||:  || || :|| | ||| :|:| : ||:|||:||
Db        113 ARLRTFAEWPRGLKQRPEELAEAGFFYTGQGDKTRCFCCDGGLKDWEPDDAPWQQHARWY 172

Qy         64 PGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMGF 123
              |:|:|  || :::  :      |  :|:     | : :
Db        173 DRCEYVLLVKGRDFVQRV----MTEACVVRDADNEPHIER-------------------- 208

Qy        124 DFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPLRRL 183
                                  :|  |||
Db        209 --------------------PAVEAEVAD------------------------------ 217

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVF 234
              ::||||||:     | |:||||:| | :||  |  ||:|   :|   |::
Db        218 --DRLCKICLGAEKTVCFVPCGHVVACGKCAAGVTTCPVCRGQLDKAVRMY 266
```

RESULT 10
A53989
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis
C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
C;Accession: A53989
R;Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A;Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po
A;Reference number: A53989; MUID:94187094; PMID:8139034
A;Accession: A53989
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <BIR>
A;Cross-references: GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g456114
A;Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Query Match 24.7%; Score 312.5; DB 2; Length 268;
Best Local Similarity 27.7%; Pred. No. 1.7e-17;
Matches 64; Conservative 31; Mismatches 57; Indels 79; Gaps 4;

```
Qy          6 ARLITFGTWMYSVNK--EQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKWY 63
              ||| ||  |   : :  |:|| |||:  || || :|| | ||| :|:| : ||:|||:||
Db        113 ARLRTFAEWPRGLKQRPEELAEAGFFYTGQGDKTRCFCCDGGLKDWEPDDAPWQQHARWY 172

Qy         64 PGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMGF 123
              |:|:|  || :::  :      |  :|:     | : :
Db        173 DRCEYVLLVKGRDFVQRV----MTEACVVRDADNEPHIER-------------------- 208

Qy        124 DFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPLRRL 183
                                  :|  |||
Db        209 --------------------PAVEAEVAD------------------------------ 217

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVF 234
              ::||||||:     | |:||||:| | :||  |  ||:|   :|   |::
Db        218 --DRLCKICLGAEKTVCFVPCGHVVACGKCAAGVTTCPVCRGQLDKAVRMY 266
```

RESULT 11
T42628
neuronal apoptosis inhibitory protein 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T42628
R;Yaraghi, Z.; Diez, E.; Gros, P.; MacKenzie, A.
Mamm. Genome 10, 761-763, 1999
A;Title: CDNA cloning and the 5'genomic organization of Naip2, a candidate gene for m
A;Reference number: Z22179; MUID:99315342; PMID:10384056
A;Accession: T42628
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1447 <YAR>
A;Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PIDN:AAC73002.1
C;Genetics:
A;Gene: Naip2

Query Match 17.6%; Score 222.5; DB 2; Length 1447;
Best Local Similarity 37.0%; Pred. No. 1.8e-09;
Matches 50; Conservative 22; Mismatches 44; Indels 19; Gaps 5;

```
Qy          5 EARLITFGTW---MYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAK 61
              |||| :|  |    :  :   |: |||   |: | |||| ||| | ||:  :|||::|||
Db        160 EARLESFEDWPFYAHGTSPRVLSAAGFVFTGKRDTVQCFSCGGCLGNWEEGDDPWKEHAK 219

Qy         62 WYPGCKYLLEEKGHEYINNIHLTRSLEGALVQT---------TKKTPSLTKRISDTIFPN 112
              |:| |::|  :|  | |      :| || |  |          :: | ::   :|::| |
Db        220 WFPKCEFLQSKKSPEEIT--QYVQSYEGFLHVTGEHFVNSWVRRELPMVSAYCNDSVFAN 277
```

```
Qy        113 PMLQEAIRMGFDFKD 127
                  | :||   |||
Db        278 ----EELRMD-TFKD 287


RESULT 12
A55478
neuronal apoptosis inhibitory protein - human
N;Alternate names: NAIP
C;Species: Homo sapiens (man)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C;Accession: A55478
R;Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; Baird, S
d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A.
Cell 80, 167-178, 1995
A;Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi
A;Reference number: A55478; MUID:95112344; PMID:7813013
A;Accession: A55478
A;Molecule type: mRNA
A;Residues: 1-1232 <ROY>
A;Cross-references: GB:U19251
C;Genetics:
A;Gene: GDB:SMA@; SMA
A;Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A;Map position: 5q12.2-5q13
C;Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot
F;94-110/Domain: transmembrane #status predicted <TMM1>
F;470-477/Region: nucleotide-binding motif A (P-loop)
F;479-496/Domain: transmembrane #status predicted <TMM2>
F;476/Binding site: ATP (Lys) #status predicted
F;618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             16.6%;  Score 209.5;  DB 2;  Length 1232;
  Best Local Similarity   34.8%;  Pred. No. 1.6e-08;
  Matches   47;  Conservative   25;  Mismatches   44;  Indels   19;  Gaps    5;

Qy          5 EARLITFGTWMY---SVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAK 61
              |||| :|  | :    ::   |: |||   |::| |||| ||| | ||:  :|||::|||
Db        160 EARLASFRNWPFYVQGISPCVLSEAGFVFTGKQDTVQCFSCGGCLGNWEEGDDPWKEHAK 219

Qy         62 WYPGCKYLLEEKGHEYINNIHLTRSLEGALVQT---------TKKTPSLTKRISDTIFPN 112
              |:| |::|  :|  | |      :| :| :  |          :: |  :   :|:||
Db        220 WFPKCEFLRSKKSSEEIT--QYIQSYKGFVDITGEHFVNSWVQRELPMASAYCNDSIF-- 275

Qy        113 PMLQEAIRMGFDFKD 127
                | :|:   |||
Db        276 --AYEELRLD-SFKD 287


RESULT 13
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C;Accession: T03183
R;Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834; MUID:98141693; PMID:9482589
A;Accession: T03183
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 <BAH>
A;Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94481.1; PID:g2738454
C;Superfamily: RING finger homology
F;159-202/Domain: RING finger homology <RRN>

  Query Match             16.2%;  Score 205;  DB 2;  Length 208;
  Best Local Similarity   26.6%;  Pred. No. 4.3e-09;
  Matches   59;  Conservative   27;  Mismatches   72;  Indels   64;  Gaps    7;

Qy          4 YEARLITFGTWMYSV--NKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAK 61
              |: || :|  |   :  :||||:||||  :   |:||||:|   |  ||  ::|:|:| |

Db         37 YDERLNSFQNWPIQLLPSKEQLSRAGFIYLNIGDQVQCFYCDLKLKEWKRSDNPFEEHKK 96

Qy         62 WYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRM 121
                |              |    :|:|           :  |  |:: | ||:
Db         97 HTQDLKI----------NCLFVKSIE---------FDNFVKNHSESCFQNPI------- 129

Qy        122 GFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPLR 181
                          |:  |         ||   |      :|:| |   :
Db        130 ---------------TNNIN--------QDLDHNQDLDHNQDLDQNSTTSDC------- 158

Qy        182 RLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMC 223
              :   ||||    |  | |||||  :| :|   :  ||:|
Db        159 ---DVLTCKICFTNKITKVLIPCGH-SSCYECVFKLQTCPIC 196


RESULT 14
T30489
apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T30489
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R
Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantri
A;Reference number: Z20836; MUID:99124785; PMID:9887315
A;Accession: T30489
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-155 <KUZ>
A;Cross-references: EMBL:AF081810; PIDN:AAC70325.1

  Query Match             15.9%;  Score 200.5;  DB 2;  Length 155;
  Best Local Similarity   22.8%;  Pred. No. 6.8e-09;
  Matches   54;  Conservative   30;  Mismatches   68;  Indels   85;  Gaps    6;

Qy          1 MTGYEARLITFGTW--MYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |     || :|  |  : :    :|| ||||   ::| |:| :|   : ||    |
Db          1 MNDERRRLASFRNWSAVDAPAPAELAHAGFYCANRQDFVKCAYCHIEIGNWSIGSDAMSD 60

Qy         59 HAKWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEA 118
              | :: | |::: |                                  | ||    : |
Db         61 HKRYSPACRFVCE----------------------------LIKR---PVSP------- 81

Qy        119 IRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEE 178
                                                  |  : |  |::        | |  |
Db         82 ----------------------------------VERRDDDDEDD-------EEDSAAE 99

Qy        179 PLRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFM 235
              | |    | || :|:|    ::| || |:| |  ||: || | :| | :: : :||:
Db        100 PAR--GGELLCSVCLDAQREIMFSPCHHVVCCAPCADMVDACVVCRAPVERRVKVFL 154


RESULT 15
T28409
ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes ent
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T28409
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28409
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-150 <AFO>
A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97724.1; PID:g4049764
C;Genetics:
A;Note: MSV248

  Query Match             15.3%;  Score 193.5;  DB 2;  Length 150;
  Best Local Similarity   19.3%;  Pred. No. 2.4e-08;
  Matches   43;  Conservative   26;  Mismatches   51;  Indels  103;  Gaps    4;
```

```
Qy          5 EARLITFGTW----MYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ::|: ::  |     : :|:  |  |||:     |   ||:||  : ||    ||| :|:
Db         17 QSRINSYENWPISLFFKINR--LCEAGFFYTNIGDITVCFNCGLKIKNWLYYNDPWIEHS 74

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              || | | |::  || ::||                      |     :  |
Db         75 KWSPNCNYIIFNKGKKFIN--------------------FAKNFKHQLLYN-------- 105

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Db        106 ------------------------------------------------------------ 105

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMC 223
                    | ||  :  |: :  ||||  || :|:  : :||:|
Db        106 --------CIICNENNISYILKPCGHASTCYECSYKIYKCPVC 140
```

Search completed: June 19, 2003, 10:08:03
Job time : 20 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:04 ; Search time 80 Seconds
(without alignments)
607.839 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264
Sequence: 1 MTGYEARLITFGTWMYSVNK.....VDRCPMCSAVIDFKQRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1264	100.0	236	4	Q96P09	Q96p09 homo sapien
2	1259	99.6	236	4	Q96RW5	Q96rw5 homo sapien
3	1241	98.2	236	6	Q95M72	Q95m72 pan troglod
4	1237	97.9	236	6	Q95M71	Q95m71 gorilla gor
5	1025	81.1	496	11	Q9ESF0	Q9esf0 rattus norv
6	1015	80.3	501	11	Q9EQ05	Q9eq05 rattus norv
7	1011	80.0	501	11	Q9EQ04	Q9eq04 rattus norv
8	678.5	53.7	493	13	Q8UVF8	Q8uvf8 gallus gall
9	497.5	39.4	628	13	Q8UWD2	Q8uwd2 brachydanio
10	465	36.8	610	13	O57319	O57319 gallus gall
11	452.5	35.8	106	4	Q96RW6	Q96rw6 homo sapien
12	445.5	35.2	602	11	Q9ESE9	Q9ese9 rattus norv
13	445	35.2	589	11	Q9ESE8	Q9ese8 rattus norv
14	445	35.2	589	11	Q9QZC6	Q9qzc6 rattus norv
15	432	34.2	405	13	Q8UWH2	Q8uwh2 brachydanio
16	401	31.7	498	5	Q960U3	Q960u3 drosophila
17	376.5	29.8	280	4	Q9HAP7	Q9hap7 homo sapien
18	373.5	29.5	298	4	Q9H2A8	Q9h2a8 homo sapien
19	373.5	29.5	298	4	Q96CA5	Q96ca5 homo sapien
20	325.5	25.8	403	5	Q8WRD9	Q8wrd9 ochlerotatu
21	325	25.7	438	5	Q9VUX5	Q9vux5 drosophila
22	320.5	25.4	377	5	Q9NJ07	Q9nj07 spodoptera
23	320	25.3	346	5	Q968T8	Q968t8 bombyx mori
24	317.5	25.1	281	12	Q9YNL8	Q9ynl8 choristoneu
25	311	24.6	379	5	Q9U492	Q9u492 trichoplusi
26	308.5	24.4	313	12	Q9J827	Q9j827 spodoptera
27	305	24.1	261	12	Q9QES9	Q9qes9 epiphyas po
28	305	24.1	276	12	O89744	O89744 buzura supp
29	300.5	23.8	402	5	Q8T621	Q8t621 aedes albop
30	289.5	22.9	264	12	Q9EN27	Q9en27 amsacta moo
31	283.5	22.4	268	12	Q9E232	Q9e232 helicoverpa
32	282	22.3	276	12	Q8QL95	Q8ql95 mamestra co
33	280.5	22.2	268	12	Q9IFI8	Q9ifi8 helicoverpa
34	249	19.7	109	6	Q8WMY4	Q8wmy4 bos taurus
35	233	18.4	243	12	Q91EW1	Q91ew1 cydia pomon
36	229	18.1	195	13	Q9IA70	Q9ia70 gallus gall
37	229	18.1	197	13	Q9IA69	Q9ia69 gallus gall
38	227.5	18.0	374	11	Q921N0	Q921n0 mus musculu
39	224	17.7	597	11	Q9R015	Q9r015 mus musculu
40	205	16.2	208	12	O55770	O55770 chilo iride
41	200.5	15.9	155	12	Q9YMI9	Q9ymi9 lymantria d
42	197.5	15.6	275	12	Q91ET9	Q91et9 cydia pomon
43	196.5	15.5	210	4	Q9BQV0	Q9bqv0 homo sapien
44	193.5	15.3	150	12	Q9YVJ4	Q9yvj4 melanoplus
45	192	15.2	292	12	O92394	O92394 bombyx mori

ALIGNMENTS

RESULT 1
Q96P09
ID Q96P09 PRELIMINARY; PRT; 236 AA.
AC Q96P09;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Testis-specific inhibitor of apoptosis.
GN BIRC8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Korneluk R.G., Lagace M.C.;
RT "Genomic Organization of the X-linked Inhibitor of Apoptosis and
RT Identification of a Novel Testis-Specific Transcript.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF420440; AAL30369.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
KW Zinc-finger.
SQ SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;

Query Match 100.0%; Score 1264; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.7e-95;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy         121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Qy         181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 2
Q96RW5
ID   Q96RW5      PRELIMINARY;      PRT;   236 AA.
AC   Q96RW5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   IAP-like protein 2.
GN   ILP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mir S.S., Duckett C.S.;
RT   "Molecular cloning of human homologs of IAP-like protein.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF164682; AAK81892.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
KW   Zinc-finger.
SQ   SEQUENCE   236 AA;  27089 MW;  DF3A170E0DDFAD9D CRC64;

  Query Match             99.6%;  Score 1259;  DB 4;  Length 236;
  Best Local Similarity   99.6%;  Pred. No. 9.4e-95;
  Matches  235;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQEEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 3
Q95M72
ID   Q95M72      PRELIMINARY;      PRT;   236 AA.
AC   Q95M72;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   IAP-like protein 2.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286921; PubMed=11390657;
RA   Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA   Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA   Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT   "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT   apoptosis protein family.";
RL   Mol. Cell. Biol. 21:4292-4301(2001).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AY030052; AAK49776.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
KW   Zinc-finger.
SQ   SEQUENCE   236 AA;  27136 MW;  64CCA3A251420EDE CRC64;

  Query Match             98.2%;  Score 1241;  DB 6;  Length 236;
  Best Local Similarity   97.9%;  Pred. No. 2.7e-93;
  Matches  231;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTGYEARLITFGTWMYFVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRINDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENESNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||:|||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        181 RRLQDEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236


RESULT 4
Q95M71
ID   Q95M71      PRELIMINARY;      PRT;   236 AA.
AC   Q95M71;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   IAP-like protein 2.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286921; PubMed=11390657;
RA   Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA   Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA   Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT   "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT   apoptosis protein family.";
RL   Mol. Cell. Biol. 21:4292-4301(2001).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AY030053; AAK49777.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
KW   Zinc-finger.
SQ   SEQUENCE   236 AA;  27120 MW;  C3A70E39EE442E4C CRC64;
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  Query Match           97.9%;  Score 1237;  DB 6;  Length 236;
  Best Local Similarity  97.0%;  Pred. No. 5.8e-93;
  Matches  229;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |||||| |||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db          1 MTGYEAWLITFGTWMYSVNKEQLARAGFYAIGQEDKIQCFHCGGGLANWKPKEDPWEQHA 60

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||||||:||||||:|||||||||||||||||||||||||||||| ||||||||||||||
Db        121 MGFDFKDIKKIMEEKIQTSGSNYKTLEVLVADLVSAQKDTTENESNQTSLQREISPEEPL 180

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||||||||||:|||||||||||||||||||||||||||:||||||||||||
Db        181 RRLQEEKLCKICMDRHIAVVFIPCGHLVTCKQCAEAVDRCPMCNAVIDFKQRVFMS 236


RESULT 5
Q9ESF0
ID   Q9ESF0      PRELIMINARY;      PRT;   496 AA.
AC   Q9ESF0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Inhibitor of apoptosis protein 3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT   "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT   Apoptosis Protein 1, 2, and 3 Genes.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF183429; AAG22969.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
KW   Zinc-finger.
SQ   SEQUENCE   496 AA;  56117 MW;  9BEF142AAEC5B798 CRC64;

  Query Match           81.1%;  Score 1025;  DB 11;  Length 496;
  Best Local Similarity  76.6%;  Pred. No. 2.5e-75;
  Matches  180;  Conservative   33;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  |:||::|||||:||||||||||||||:|: |||:||||||||| :||| ||||||||
Db        261 MAEYDARIVTFGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:||| |||||||| ||  ::|:| :||||:||:| |||| |||:|||||
Db        321 KWYPGCKYLLDEKGQEYINNIHLTHSLGESVVRTAEKTPSVTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||:|||:|| |||::|||||| :||||:||||||| :::| :|||||::|| || |
Db        381 MGFNFKDIKKTMEEKLQTSGSNYLSLEVLIADLVSAQKDNSQDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFM 235
              |||||||||||||| ||:||:|||||||||||||||:|||  || |||::||
Db        441 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCCTVITFKQKIFM 495


RESULT 6
Q9EQ05
ID   Q9EQ05      PRELIMINARY;      PRT;   501 AA.
AC   Q9EQ05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Inhibitor of apoptosis protein 3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=OVARY;
RA   Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT   "Cloning, characterization and regulation of an inhibitor of apoptosis
RT   protein in the rat corpus luteum.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF304333; AAG41192.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
KW   Zinc-finger.
SQ   SEQUENCE   501 AA;  56548 MW;  0973FBF28E81C5A0 CRC64;

  Query Match           80.3%;  Score 1015;  DB 11;  Length 501;
  Best Local Similarity  77.2%;  Pred. No. 1.7e-74;
  Matches  179;  Conservative   32;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  |:||::|||||:||||||||||||||:|: |||:||||||||| :||| ||||||||
Db        261 MAEYDARIVTFGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLADWKPSEDPWEQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:||| |||||||| ||  ::|:| :||||:||:| |||| |||:|||||
Db        321 KWYPGCKYLLDEKGQEYINNIHLTHSLGESVVRTAEKTPSVTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||:|||:|| |||::|||||| :||||:||||||| :::| :|||||::|| || |
Db        381 MGFNFKDIKKTMEEKLQTSGSNYLSLEVLIADLVSAQKDNSQDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQR 232
              |||||||||||||| ||:||:|||||||||||||||:|||| || |||:
Db        441 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCCTVITFKQK 492


RESULT 7
Q9EQ04
ID   Q9EQ04      PRELIMINARY;      PRT;   501 AA.
AC   Q9EQ04;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Inhibitor of apoptosis protein 3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=OVARY;
RA   Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT   "Cloning, characterization and regulation of an inhibitor of apoptosis
RT   protein in the rat corpus luteum.";
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RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF304334; AAG41193.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
KW   Zinc-finger.
SQ   SEQUENCE   501 AA;  56578 MW;  4863F69FF2E0C8CD CRC64;

  Query Match             80.0%;  Score 1011;  DB 11;  Length 501;
  Best Local Similarity   76.7%;  Pred. No. 3.5e-74;
  Matches  178;  Conservative   32;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  |:||::|||||:||||||||||||||||:|: |||:|||||||| :||| ||||||||
Db        261 MAEYDARIVTFGTWLYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||||||||||:||| |||||||||  ||  ::|:| :||||:||:| |||| |||:|||||
Db        321 KWYPGCKYLLDEKGQEYINNIHLTHSLGESVVRTAEKTPSVTKKIDDTIFQNPMVQEAIR 380

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPL 180
              |||:|||:|| |||::|||||||| :||||:||||||||| :::| :||||||:|| || |
Db        381 MGFNFKDIKKTMEEKLQTSGSNYLSLEVLIADLVSAQKDNSQDESSQTSLQKDISTEEQL 440

Qy        181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQR 232
              |||||||||||||| ||:||:||||||||||||||||:|||| || |||:
Db        441 RRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCCTVITFKQK 492


RESULT 8
Q8UVF8
ID   Q8UVF8      PRELIMINARY;      PRT;   493 AA.
AC   Q8UVF8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Inhibitor of apoptosis protein 3.
GN   IAP3.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bridgham J.T., Johnson A.L.;
RT   "Identification of chicken inhibitor of apoptosis protein XIAP
RT   (IAP3).";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF451854; AAL47170.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   493 AA;  55251 MW;  030A9F56CB6119BC CRC64;

  Query Match             53.7%;  Score 678.5;  DB 13;  Length 493;
  Best Local Similarity   52.5%;  Pred. No. 3.9e-47;
  Matches  124;  Conservative   43;  Mismatches   64;  Indels    5;  Gaps    3;

Qy          1 MTGYEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHA 60
              |  || |: ||  |:| |||| || ||||: |  | | ||||||||  ||  ||||:|||
Db        261 MAEYERRIQTFLAWIYPVNKEHLAEAGFYSTGNGDHVVCFHCGGGLQEWKENEDPWDQHA 320

Qy         61 KWYPGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIR 120
              ||:||||:| :||| |:|||:||      : ::  : |  | |   | :  | ::| ||
Db        321 KWFPGCKFLRDEKGLEFINNVHLRDGCRDSTIEAAEVT-ILPK---DDLLQNQLVQNAIH 376

Qy        121 MGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE-LNQTSLQREISPEEP 179
              |||   ::: |||:::  || :| ::| |||||:||||:  : |   :: |::::| ||
Db        377 MGFSLSEIRSIMEKKLHLSGESYTSVEDLVADLISAQKENIKGEPPKESPLEQDLSIEEK 436

Qy        180 LRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFM 235
              |||||||||||||| : |:|| ||||||| ||:|||||::||:|   |  :|::||
Db        437 LRRLQEEKLCKICMAKDISVVLIPCGHLVACKECAEAVNKCPLCCTNIIKRQKIFM 492


RESULT 9
Q8UWD2
ID   Q8UWD2      PRELIMINARY;      PRT;   628 AA.
AC   Q8UWD2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Iap1.
GN   IAP1.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20373792; PubMed=10917738;
RA   Inohara N., Nunez G.;
RT   "Genes with homology to mammalian apoptosis regulators identified in
RT   zebrafish.";
RL   Cell Death Differ. 7:509-510(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Inohara N., Nunez G.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF442500; AAL33679.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   628 AA;  70098 MW;  5B68CEB6A87C8A95 CRC64;

  Query Match             39.4%;  Score 497.5;  DB 13;  Length 628;
  Best Local Similarity   30.9%;  Pred. No. 2.8e-32;
  Matches  108;  Conservative   47;  Mismatches   77;  Indels  117;  Gaps    6;

Qy          5 EARLITFGTW--MYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKW 62
              | ||:|| |     |  :|||:|||| :|: | |:|| | |||  |:  :||| :||||
Db        280 EERLLTFVNWPSRIPVRPDQLAKAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKW 339

Qy         63 YPGCKYLLEEKGHEYINNI--HLTRSLEGALVQTTKKT-----------PSLTKRISDT 108
              :| |:|||:||| |::: |     |  |  |     .           |   :
Db        340 FPRCEYLLQEKGQEFVHQIQARFPRLFEQLLTNGDSNSREFVDPPVVHLGPGEDRSEDAV 399

Qy        109 IFPNPMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENE---- 164
              :  ||::: |: |||:   ||: :: :| ||| ||||:: ||:||:||: :  | |
Db        400 MMNNPVVKSALEMGFERGLVKQTVQSKILTSGENYKTVQELVSDLLSAEDEKREEERELL 459
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Qy        165 ------------------------------------------------------------ 164

Db        460 AEEMASDGFTFLKKHHAALSQRLKSVQSLMDHLLEENVISQKEYDSIRNCTSVKQQTGQL 519

Qy        165 -------------------LNQTSLQREI--------SP---------EEPLRRLQEEK 187
                              |   | ||:         ||          || |||||||:
Db        520 IDLVLSKGNAAAEVFRNWIKKNDVYLLRELMAQTNEAASPSQDLSDLPMEEQLRRLQEER 579

Qy        188 LCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
                ||:|||: : :|||||||| ||:|| :: :||:|  ::    | |:|
Db        580 TCKVCMDKEVNIVFIPCGHLVVCKECAPSLRKCPICRGMVKGTVRTFLS 628


RESULT 10
O57319
ID   O57319      PRELIMINARY;      PRT;   610 AA.
AC   O57319;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Inhibitor of apoptosis PROTEIN 1 (IAP) (Inhibitor of T.cell apoptosis
DE   PROTEINE).
GN   IAP1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC FIBROBLAST;
RX   MEDLINE=98038801; PubMed=9372964;
RA   You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT   "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT   mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
RL   Mol. Cell. Biol. 17:7328-7341(1997).
CC   -!- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC       CELLS.
CC   -!- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC       THE V-REL-TRANSFORMED CELLS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC       SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC       IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC   -!- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC       PROCESS.
CC   -!- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC   -!- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC       APOPTOSIS PROTEIN REPEAT).
CC   -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR   EMBL; AF008592; AAB88044.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
KW   Apoptosis; Zinc-finger; Repeat.
FT   REPEAT       30     97       BIR REPEAT 1.
FT   REPEAT      176    242       BIR REPEAT 2.
FT   REPEAT      262    329       BIR REPEAT 3.
FT   ZN_FING     563    597       C3HC4-TYPE.
SQ   SEQUENCE   610 AA;  68924 MW;  ADF47619650B44A6 CRC64;

  Query Match             36.8%;  Score 465;  DB 13;  Length 610;
  Best Local Similarity   30.3%;  Pred. No. 1.2e-29;
  Matches  108;  Conservative   48;  Mismatches   75;  Indels  126;  Gaps    9;

Qy          1 MTGYEARLITFGTW--MYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
                |  :|||: ||  |     |  |||| |||| :|: | |:|| | |||  |:  :||| :
Db        259 MQTHEARVKTFINWPTRIPVQPEQLADAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWIE 318

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSLEGALVQTTKKTP---SLTKRI----- 105
               ||||:| |:|||  || |::: :     ||    |      :|  ||   ::   |
Db        319 HAKWFPRCEYLLRVKGGEFVSQVQARFPHLLEQL-----LSTSDTPVDENMDPIIHFEPG 373

Qy        106 ----SDTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDT 160
                  | |  | |::: |: |||  : :|: :: :|  :  ||||:  ||:||::|: :
Db        374 ESPSEDAIMMNTPVVKAALEMGFSRRLIKQTVQSKILATEENYKTVNDLVSDLLTAEDEK 433

Qy        161 TENE-----------------------------------------------------LNQ 167
                | |                                                     |
Db        434 REEEKERQFEEVASDDLSLIRKNRMALFQRLTSVLPILGSLLSAKVITELEHDVIKQKTQ 493

Qy        168 TSLQ----------------------REISP-------------------------EEP 179
                | ||                    ::  |                         ||
Db        494 TPLQARELIDTVLVKGNAAASIFRNCLKDCDPVLYKDLFVEKSMKYVPTEDVSGLPMEEQ 553

Qy        180 LRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||||||: ||:|||: :::|||||||| ||:|| :: :||:|   |    | |:|
Db        554 LRRLQEERTCKVCMDKEVSIVFIPCGHLVVCKECAPSLRKCPICRGTIKGTVRTFLS 610


RESULT 11
Q96RW6
ID   Q96RW6      PRELIMINARY;      PRT;   106 AA.
AC   Q96RW6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   IAP-like protein 3.
GN   ILP3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mir S.S., Duckett C.S.;
RT   "Molecular cloning of human homologs of IAP-like protein.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF164681; AAK81891.1; -.
DR   InterPro; IPR001370; BIR.
DR   Pfam; PF00653; BIR; 1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
SQ   SEQUENCE   106 AA;  12360 MW;  6BBAD3AEA880A891 CRC64;

  Query Match             35.8%;  Score 452.5;  DB 4;  Length 106;
  Best Local Similarity   74.5%;  Pred. No. 1.5e-29;
  Matches   79;  Conservative   15;  Mismatches   11;  Indels    1;  Gaps    1;

Qy         14 WMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKWYPGCKYLLEEK 73
              |:||||||:|||||:|: |||:|||||||| :||| ||||||| ||:|||||||:|
Db          2 WIYSVNKEQLSRAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHDKWHPGCKYLLEQK 61

Qy         74 GHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAI 119
                 :|||||||: |||  ||:| :|||||||::| |||| |||:||||
Db         62 TRKYINNIHLSHSLEECLVRTAEKTPSLTRKI-DTIFHNPMVQEAI 106


RESULT 12
Q9ESE9
ID   Q9ESE9      PRELIMINARY;      PRT;   602 AA.
AC   Q9ESE9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Inhibitor of apoptosis protein 1.
OS   Rattus norvegicus (Rat).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT   "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT   Apoptosis Protein 1, 2, and 3 Genes.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF183430; AAG22970.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
KW   Zinc-finger.
SQ   SEQUENCE   602 AA;  67326 MW;  CC91385EEA62DE5A CRC64;

  Query Match           35.2%;  Score 445.5;  DB 11;  Length 602;
  Best Local Similarity   29.1%;  Pred. No. 4.5e-28;
  Matches  104;  Conservative   45;  Mismatches   81;  Indels  127;  Gaps    8;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: || ||  |  |: ::|| ||||  |  | |:|| | |||  |:  :||| :
Db        252 MQTHAARVRTFSTWPSSALVHPQELASAGFYYTGHSDDVKCFCCDGGLRCWESGDDPWVE 311

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSL----------EGALVQTTKKTPSL 101
              ||||:| |:||:  || |::  :     ||   |           | |:|
Db        312 HAKWFPRCEYLIRIKGQEFVGQVQAGYPHLLEQLLSTSDSPEDETGEAAIVHL-----GP 366

Qy        102 TKRISDTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDT 160
              :   | :  | |::: |: |||    |:: :: :|  :| ||:|:  ||  |: |: :
Db        367 GENWEDAVMMNTPVVKAALDMGFSRSLVRQTVQRQILATGENYRTVSDLVIGLLDAEDEM 426

Qy        161 TENELNQ---------------------------------------------------- 167
              | :  |
Db        427 REEQTEQEAEEEESDDLTLIRKNKMVLLQHLTPVTPILDCLLSARVITEQEYDAVKQKPH 486

Qy        168 ----------------------TSLQREISP------------------------EEP 179
                                     ||| || |                        ||
Db        487 TLQARTLIDTVLAKGNTAATSFRNSLQ-EIDPGLYRDIFVRQNIRSLPTDDIAALPMEEQ 545

Qy        180 LRRLQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||:|||: ||:|||  ::|||||||| ||:|| :: :||:|   |    | |:|
Db        546 LRKLQEERTCKVCMDREASLVFIPCGHLVVCKECAPSLRKCPICRGTIKGTVRTFLS 602


RESULT 13
Q9ESE8
ID   Q9ESE8      PRELIMINARY;      PRT;   589 AA.
AC   Q9ESE8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Inhibitor of apoptosis protein 2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT   "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT   Apoptosis Protein 1, 2, and 3 Genes.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF183431; AAG22971.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
KW   Zinc-finger.
SQ   SEQUENCE   589 AA;  66750 MW;  B4F7089BD7CD285B CRC64;

  Query Match           35.2%;  Score 445;  DB 11;  Length 589;
  Best Local Similarity   28.8%;  Pred. No. 4.8e-28;
  Matches  102;  Conservative   49;  Mismatches   83;  Indels  120;  Gaps    7;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||  |  |  |  |||| |||| :   | |:|| | |||  |:| :||| :
Db        238 MQTHSARMSTFLYWPSSVLVQPEQLASAGFYYVDHNDDVKCFCCDGGLRCWEPGDDPWIE 297

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSL---------EGALVQTTKKTPSLTKR 104
              ||||:| |::|:  || |::: |     ||   |           | |        |  :
Db        298 HAKWFPRCEFLIRMKGQEFVDEIQARYPHLLEQLLSTSDTSEEENADPPVVHLGPG--EN 355

Qy        105 ISDTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTEN 163
                | :  | |::: |: |||    |:: :: :|  :| ||:|:  :|: |::|: :  |
Db        356 WEDAVMMNTPVVKAALDMGFSRSLVRQTVQRQILATGENYRTVSDIVSALLNAEDERREE 415

Qy        164 E-----------------------------------LNQTSLQRE------------- 173
              |                                   |  : | :|
Db        416 EKERQSEETASGDLSLIRKNRMALFQQLTCVIPILDDLLEASVLTKEEHDIIRQKTQIPL 475

Qy        174 ------------------------------------------------------ISPEEPLRR 182
                                                                     :| || |||
Db        476 QARELIDTILVKGNAAASVFKNSLKEVDSTLYEHLFVEKTMKYIPTEDVSGLSLEEQLRR 535

Qy        183 LQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              |||| ||:|||| :::|||||||||| |::|| :: :||:|   |    | |:|
Db        536 LQEERTCKVCMDREVSIVFIPCGHLVVCRECAPSLRKCPICRGTIKGTVRTFLS 589


RESULT 14
Q9QZC6
ID   Q9QZC6      PRELIMINARY;      PRT;   589 AA.
AC   Q9QZC6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Inhibitor of apoptosis protein 2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT   "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF190020; AAF04585.1; -.
DR   HSSP; Q13490; 1QBH.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001315; CARD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
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DR   Pfam; PF00619; CARD; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00114; CARD; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 3.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50209; CARD; 1.
KW   Zinc-finger.
SQ   SEQUENCE   589 AA;  66777 MW;  E6812FFE3EA34142 CRC64;

  Query Match             35.2%;  Score 445;  DB 11;  Length 589;
  Best Local Similarity   28.8%;  Pred. No. 4.8e-28;
  Matches  102;  Conservative   49;  Mismatches   83;  Indels  120;  Gaps    7;

Qy          1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQ 58
              |  : ||: ||   |  |  |  |||| |||| :   | |:|| | |||  |:| :||| :
Db        238 MQTHSARMSTFLYWPSSVLVQPEQLASAGFYYVDHNDDVKCFCCDGGLRCWEPGDDPWIE 297

Qy         59 HAKWYPGCKYLLEEKGHEYINNI-----HLTRSL---------EGALVQTTKKTPSLTKR 104
              ||||:| |::|:  || |::: |     ||   |          | |          |  :
Db        298 HAKWFPRCEFLIRMKGQEFVDEIQARYPHLLEQLLSTSDTSEEENADPPVVHLGPG--EN 355

Qy        105 ISDTIFPN-PMLQEAIRMGFDFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTEN 163
                | :  | |::: |: |||    |:: :: :|  :| ||:|:  :|: |::|: :  |
Db        356 WEDAVMMNTPVVKAALDMGFSRSLVRQTVQRQILATGENYRTVSDIVSALLNAEDERREE 415

Qy        164 E-----------------------------------LNQTSLQRE------------ 173
              |                                   |  : | :|
Db        416 EKERQSEETASGDLSLIRKNRMALFQQLTCVIPILDDLLEASVLTKEEHDIIRQKTQIPL 475

Qy        174 ------------------------------------------------ISPEEPLRR 182
                                                             :| || |||
Db        476 QARELIDTILVKGNAAASVFKNSLKEVDSTLYEHLFVEKTMKYIPTEDVSGLSLEEQLRR 535

Qy        183 LQEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVFMS 236
              ||||: ||:|||| :::|||||||||| |::|| :: :||:|   |    | |:|
Db        536 LQEERTCKVCMDREVSIVFIPCGHLVVCRECAPSLRKCPICRGTIKGTVRTFLS 589


RESULT 15
Q8UWH2
ID   Q8UWH2      PRELIMINARY;      PRT;   405 AA.
AC   Q8UWH2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Xiap.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20373792; PubMed=10917738;
RA   Inohara N., Nunez G.;
RT   "Genes with homology to mammalian apoptosis regulators identified in
RT   zebrafish.";
RL   Cell Death Differ. 7:509-510(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Inohara N., Nunez G.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF439767; AAL32047.1; -.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 3.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00238; BIR; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50143; BIR_REPEAT_2; 3.
DR   PROSITE; PS50089; ZF_RING_2; 1.

SQ   SEQUENCE   405 AA;  45564 MW;  A366E342D83BECAB CRC64;

  Query Match             34.2%;  Score 432;  DB 13;  Length 405;
  Best Local Similarity   36.4%;  Pred. No. 3.5e-27;
  Matches   84;  Conservative   38;  Mismatches   53;  Indels   56;  Gaps    4;

Qy          4 YEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKPKEDPWEQHAKWY 63
              :| || :|    : :: |:|||||||: |::|:| || ||||:  | | |||||:||: |
Db        229 FEGRLDSFKGRQHPIDPERLARAGFYSTGEQDRVMCFRCGGGVKAWMPDEDPWEEHARHY 288

Qy         64 PGCKYLLEEKGHEYINNIHLTRSLEGALVQTTKKTPSLTKRISDTIFPNPMLQEAIRMGF 123
              ||| :|| ||| ||:::: |                          :|    |    ||
Db        289 PGCSFLLAEKGEEYVSSVQLR------------------------YPKRPTQN----GF 319

Qy        124 DFKDVKKIMEERIQTSGSNYKTLEVLVADLVSAQKDTTENELNQTSLQREISPEEPLRRL 183
                :           |||: : |    :|:   :|                |   | :|
Db        320 SSHE----------SGSSAQALIHGSSDMFEKAED---------------PMTELEKL 352

Qy        184 QEEKLCKICMDRYIAVVFIPCGHLVTCKQCAEAVDRCPMCSAVIDFKQRVF 234
              | |||||:|||  |::|||||||||||::|: ::|:||:| | |  | : :
Db        353 QREKLCKVCMDSDISIVFIPCGHLVTCQKCSASLDKCPICCATITQKIKTY 403


Search completed: June 19, 2003, 10:09:31
Job time : 83 secs
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